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Minimum DB seq length: 0
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS	MS	ACCESSION VERSION KEYWORDS	RESULT 1 AE004352/c LOCUS DEFINITION
<pre>vibrionaceae; vibrio. 1 (bases 1 to 10977) 1 (bases 1 to 10977) Heidelberg, J. F., Eisen, J. A., Nelson, W. C., Clayton, R. A., Gwinn, M. L., Dodson, R. J., Haft, D. H., Hickey, E. K., Peterson, J. D., Umayam, L.,</pre>	Vibrio cholerae Ol biovar eltor str. N16961 Vibrio cholerae Ol biovar eltor str. N16961 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	9 of 93 of the complete chromosome. AE004352 AE003853 AE004352.1 GI:9657475	AE004352 10977 bp DNA linear BCT 10-OCT-2003 Vibrio cholerae Ol biovar eltor str. N16961 chromosome II, section

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JOURNAL
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DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Location/Qualifiers
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//db_xref="G1:9657484"
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//ta_sref="G1:9657484"
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suddlkabiergdonussitemotrarssovvalcruvachkosiepowilgisynybar
sedixco-g67134Empmodoalvmensoovvalcruvachkosiepowilgispodalelc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VCA0100"
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/gene="VCA0100"
/note="similar to GP:72
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RQRWREQAQEGGGILPDLAPHLLDQALVLFGLPQSLSADCRMMR.PDATTLDYFDLQLY
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YPQHVVRLHANLYSPEPNVRYQVLGSLGKYVKYGLDPQEDRLKAGER.PTHPQWSQEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="VCA0099"
/note="similar to GB:U00096 PID:1742678 PID:1742686
PID:1742694 PID:1742718; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="VCA0099"
7856. .8896
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/note="similar to GB:J05568 SP:P18133 PID:147307 GB:U00096
PID:1651456; identified by sequence similarity; putative"
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/transl_table=11
/product=roxidoreductase, Gfo/Idh/MocA
/protein_id="AAP96013.1"
/db_xref="GI:9657485"
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Submitted (13-DEC_2002) Department of Microbiology, Genome Research Center for Enteropathogenic Bacteria, Chonnam National University Medical School, Hak-1-Dong, Dong-Gu, Kwang-Ju 501-746, South Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-DEC-2002) Genotech Corp., 461-6, Jeonmin-dong, Yuseong-gu, Daejeon 305-811, South Korea 3 (bases 1 to 306147)
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Kim,Y.R., Lee,S.E., Kim,C.M., Kim,S.Y., Schung,S.S., Choy,H.E., Progulske-Fox,A.,
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NGGLHPVTRTVERIEQFFGELGFNVESGPEIEDAFHNFDALNIAADHPARTDHDTFFF
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                                                                                                                                                                                                                            NFAQLKGILHDFLCNFFEEEVEVRFRPSYFPFTEPSAEVDVKGKMGKWLEVLGCGMVH
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ske-Fox,A., Hillman,J.D., Handfield,M.
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GEYFAGRAQISFGIGTFLANDMGNWTNDKGTRYQPISMVVKMAECNGSFVAKISDEPE
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962. .7249
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602 ACHARCTAGTCAGTCAGTCAGTTATTTAGCCTTATTATATTATGGATATTGAGGGGTAAGG 4989 ACTAACATCCAATGCTCTGGCGAGGGATCCCGGCCTAATTTGATTCTTATTTTTTTT	4707 GCGAGGGTTGATTCCTCACGAACCTCTACACTAAATCAAATCAAATCAAATCAAATCAAACGAACTATCATACAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAAATCAAATCAAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATAAAAAA	65 CGGCTACGTACTTCAGAGATTAAAGGCCATGACTAGCGTTTCATAAAAATGGTGTCTCGC 124

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen,C.Y., Wu,K.M., Chang,Y.C., Chang,C.H., Tsai,H.C., Liao,T.L.,
Liu,Y.M., Chen,H.J., Shen,A.B., Li,J.C., Su,T.L., Shao,C.P.,
Lee,C.T., Hor,L.I. and Tsai,S.F.
Comparative Genome Analysis of Vibrio vulnificus, a Marine Pathogen
Genome Res. 13, 2577-2587 (2003)
2 (bases 1 to 24190)
Chen,C.Y., Wu,K.M. and Tsai,S.F.
Direct Submission
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AP005337.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-MAY-2002) Shih Feng Tsai, National Health
Institutes, Division of Molecular and Genomic Medicine,
Yen-Chiu-Yuan Road, Sec 2, Taipei, Taiwan 115, Republic
(E-mail:petsai@nhri.org.tw, Tel:886-2-8146-1041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP005337
Vibrio vulnificus
                                                                                                                                                                                                                                                                                                                                             http://genome.ym.edu.tw).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Fax:886-2-2789-0484)
This sequence was de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio vulnificus YJ016
                                                                                                                                                                                                                                                                                                                                                                                    This sequence was determined by the Sequencing Core Yang-Ming University Genome Research Center (YMGC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'ibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACATCGGTGGTCTTGTTTGCACTCGAAAAAAGAGTTTCTCGTTTCTGACATCATTCACGC
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genome, section
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GLRSVENRTLTDDIITIENNKFLANSTVYVGNYGALDMQVIPFYVGMDEIVLAREI
GLRSVENRTLTDDIITIENNKFLANSTVYVGNYGALDMQVIPFYVGMDEIVLAREIVLAREIVLANSTVYVGNYGALDMQVIPFYVGMDEIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIVLAREIV
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YTTANTADF!VVGGPKADPAKVAQDNSVLEVFKALADNAVPTSISGDDSGTHKKZELGIWGPK
MYXHDF!VVGGPKADPAKVAQDNSVLEVFKALADNAVPTSISGDDSGTHKKZELGIWGF
KMFDFFFKADFAKVADVAKVADKSENGENTATTSTYLDRGTWLAVNAKLDLAVLFEGDQKLFN
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LAMQSSLLRVLEQRSIRPVGSEKEIPVDVRVVAATNRDLQQEVEKGRFRKDLYYRLNV
LKIEVPPLRERKADLQELVPFFTKQLSGELAMSAPQMAHEDIEAMHDYSWPGNVRELR
                                                                                                                                                                                                                                                                                                                                                                                       PYQVILVNPERYPSINYQGAKAFSDWLVNPRGQELINSFRLNGKQLFVANADQK"
12767. .13465
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11942. .12760
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/gene="VV1711"
/codon_start=1
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/gene="VV1711"
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/gene="V1713"
/codon_start=1
/trans1_table=11
/product="ABC-type tungstate transport
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11942. .12760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="sigma-54 dependent response regulator"
/protein_id="BAC94476.1"
/db_xref="GI:37198642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (10173. .11678)
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                                                                                                                     /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                    /gene="W1714"
                                                                                                                                                                                                                                                                                                                                          12767. .13465
/gene="VV1714"
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/transl_table=
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AGTTCTGCTGATTAAGCGCACCAATCCTGAGAGACCACAGCATGGCATGTGGTCTATTCC
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                                           GGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGTAAATGGGCATTGCC
                                                                                                  TIGCCGTATGATTGTTACGATTGACATGATTTGCCTGAAGCTAGGTGAGAAAGGGCTGGA
                                                                                                                                                   AGCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTTGCGCCGAAATCTATCCA
                                                                                                                                                                                                    CTTTCCTATTGACCCTATAGGATCGTCTCAGTATTGTAGTGCCAGTTTGATGTTTAAGAG
                                                                                                                                                                                                                                                     TTATTTACATTTGACCATCATCATGCACTTACCTAAAATAAGCCCCGTTGTTTATTAGGGA
                                                                                                                                                                                                                                                                                                        GATAAAGCATGCCTGGAATTGAATGATTAGGTATAAATCAAAGTTAGGAACAAAAGTGTA
                                                                                                                                                                                                                                                                                                                                                    ACGTAGTCATAACAATTACAGTACTCTTGTTATCTGAGTTATGTTTGTCACAAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                        ACTAACACCCCATGGTTTGGCGAGGTAGCTACCAGGCTAATTTGATTCTTATGTTTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAACCTAGTCAGTCGTTATTTGGCCTTATTATAATTA--TGGATATTGAGGGGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTGTTCGTTAATGTGCT-GAACTCTAAATGAGAGAGAGTATGGTTTGTCAATTTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGTGTTGCTAACTTTGGGCGAACAATAAAGTACCCTTGTAAGTTTGTCAACTTTTGTG
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FLSFLLAYTWERGKMILVSEVNTLQSVPTVVIGLLLYMFLSKSGPLGDWQMLFTQKAM
ILGQMLICEPVLVSMMYGALQSSDRRALETALTLGVSLPRLSATMIWETRFPLMAATI
TGFSRIVTEVGCSMMYGGNIMGITRNIPTAISMESHKGAFAQGVALGIVLLTLALVLN
FLLSSMGKCYLRT"
13474...14193
/gene="VV1715"
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Pred. No. 8.2e-124;
0; Mismatches 593;
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Vibrio parahaemolyticus DNA,
AP005085 BA000032
3 (bases 1 to 303450)
Oshima, K., Kurokawa, K.,
Honda, T., Shinagawa, H.,
                                                                                                     Genome sequence of Vibrio parahaemolyticus: distinct from that of V cholerae Lancet 361 (9359), 743-749 (2003)
                                                                                                                                                               Makino,K., Oshima,K., Kurokawa,K., Yokoyama,K., Uda,T., Tagomori,K., Iijima,Y., Najima,M., Nakano,M., Yamashita,A., Kubota,Y., Kimura,S., Yasunaga,T., Honda,T., Shinagawa,H., Hattori,M. and Iida,T.
                                                                                                                                                                                                                                                                                                         Makino,K., Shinagawa,H. and Honda,T.
A filamentous phage associated with recent pandemic Vibrio parahaemolyticus O3:K6 strains
J. Clin. Microbiol. 38 (6), 2156-2161 (2000)
                                                                                                                                                                                                                                                                                                                                                                                           Nasu, H.,
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Vibrio parahaemolyticus
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
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        Makino, K.,
Hattori, M.
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        Yokoyama, K., and Iida, T.
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                                                                                                                                                pathogenic mechanism
                              Yasunaga, T.,
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This clone was
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Information Research Center: 3-1, Yamadaoka, Suita, Osaka 5
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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2974. .3714
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#PTQNRABEKLVQELYYQRAIGAYYQMQPAMAVIGKRDGSESKEKGYNVLPIWGDKM
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QLPNGAPESNYIKTIPGRDFLTAIRLYGTGIEFFDQTWKPDDVLKIK"
complement (1835. . .2314)
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                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mmekiyfaggclwgvqefmrhlpgvisteagrangktdniqsey
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/transl_table=11
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identity 68 in 487 aa"
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                 note≖"similar to
                                                                                                                                                                                                                                                                                                                   note="gimilar to
                                                                                                                                                                                                                                                                                                                                       gene="VPA0302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .303450
                                                                                                                                                                                                                                                                                                in 129 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="taxon:670"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            experimental
               GB:AAL20622.1 (AE008775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DBJ:BAB43758.1
                                                                                                                                                                                                                                                                                                                      GB:AAA64344.1 (L16865) percent identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AP003138)
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/product="catalase"
/db_xxef="gatalase"
/db_xx
                                                                                                                                                                                                                                                                                                /product="AnkB protein"
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/dbcein id="BAC61649.1"
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GNNEVVETFVSQGFPIDQRNNBSYTALMVAAYQGNKDTVRLLLDSGANACLQDKRGNT
GNNEVVETFVSQGFPIDQRNNBSYTALMVAAYQGNKDTVRLLLDSGANACLQDKRGNT
ALMGALIKREISIAKDLYQAECSDLKNKAGLDLKTFAEIYGQSEVLKSLQNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="VPA0306"
5962. .6429
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Gylkryhgaafalqsddidtrleyrpdkgytgytkaadlyapustylieggsanalla
Rtlaergdytiitbasiitiesaitalliknisaniillicgyyqhgesilygplyrlcienihes
Taflgidgfhqdtgftsrdmyradiaeailakkrrniyltdsskfgqiypssigktne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to Cidentity 63 in 152 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MHQHEKLNYVEFGTPNIGATKAFFEHVFGWQFVDYGFDYAAFSG
QGLDGGFYSAEQVSQTSNGAALLVFYSSDIHATLEKVAKFGGQIIRPIFEFPGGCRFH
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/evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                    complement (6548. .7201)
                                                                                                                                                                                                                                                                       complement (6548. .7201)
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                                                                                                  /gene="VPA0307"
/note="similar to GB:AAF42465.1
identity 47 in 200 aa"
                                                                                                                                                                                                                                    /gene="VPA0307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to REF:NP_231225.1 (NC_002505) percent
identity 83 in 510 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTEPSGNEFAVWSESH"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="VPA0305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="VPA0305"
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/db_xref="GI:28808470"
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dentity 76 in 117 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="VPA0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                          CTAACCACTCTTTTTATATGGTTTTTCCGTTTAAAAATTCAGCACTGATTGTGAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAATTTGCCGATCGGGTTGAAAATGGGAAATAGCGTAATGACTGTAAAAAAGTACGAT
                                                                                                         CAAACCTAGTCAGTCGTTATTTGGCCTTATTATAATTATGGATATTGAGGGGTAAGGACG
                                                                                                                                                                                                               ACGTGTTGCTAACTTTGGGCGAACAATAAAGTACCCTTGTAAGTTTTGTCAACTTTTTGTGA
                                                                                                                                                                                                                                                                                                          TGGTCGTCATTCGGAGCCCTTCTACATGCCCTTCCGTGGGTATATAACTTTTTGTTACTA
                                                                                                                                                                                                                                                                                                                                                                          TATTGATTTTATAGGCATCAAGATCCAATAAACTGCGGATAAAAAGAGGGAGAAAATAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGTTTAAGAACTTCTGCCTTTACCTCTGGCAGCAATTCCGACAGATCTTCTTCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAACTGATTGATTTCTTGGCGTACTTCCTCTAATAAATCGCTAATGTCTTCATCACTGC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAATGAGGTGCATGCTGCTCTAAATAAACAATGTCGGCATCCGAAAAGCGCAATGAAG
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gene SgS

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6 GCACTTTATCAGCCAATACTTGCATCGGTAACTCGGCGGGCACTTGTGCCCAGTGGCGGC
                                                   Conservative
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GKPAMVYTLTSDEVTFFQNCLRG"
                                                                                                                                                                                            /translation="MIVTVDIIPFRLSGCADKGLEVLLIKRSNENREYHGVWALEGGF
VFDKDLTSEGGRPADENFEAARRICREKIHTYPRHFSEAFIDGDPKRDPEDWSLNIT
HYALVDRNNVEQINNAGVPECQLKWFPLQAILNGEETLAFDHQKTIEKAWQKLRASIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTVRVNYQTTAVIDVDPEKGFSELCPDELPVAGALDIVPELLKN HAKGRLKIVSRDLHPVKAAMDAETPANMLEPVGLPNVDVKWNRHCVLGTTGVELLDGL PPVLDYDFQVNKGMDEDAHPVGIFFHDVADTKTTGANEFLKCNKIDTVVVGGLALDFC VKKSVMQALDLGFKVIVNLAATRAVLFDTVDSVIAEMKEKGALFVKNADDIIVERFA" complement (7234. .7959) /gene="VPA0308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7234. .7959)
                                                                                                                                                                                                                                                               /product="conserved hypothetical
/protein_id="BAC61651.1"
/db_xref="GI:28808474"
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/protein_id="BAC61650.1"
/db_xref="GI:28808473"
                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                      evidence=not
                                                                                                                                                                                                                                                                                                                                                                                                                    dentity 60 in 241 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                              note="similar
                                                                     15.6%;
                                                      0
                                                                        Score 403; DB 1;
Pred. No. 2.4e-106;
                                                                                                                                                                                                                                                                                                                                                                      experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                         to GB:AAF96011.1
                                                      Mismatches
                                                                                            Length 303450;
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Vibrio vulnificus YJ016
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This sequence was determined by the Sequencing Core of tyang-Ming University Genome Research Center (YMGC;
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Liu, Y.M., Chen, H.J., Shen, A.B., Li, J.C., Su, T.L., S
Lee, C.T., Hor, L.I. and Tsai, S.F.
Comparative Genome Analysis of Vibrio vulnificus, a
Genome Res. 13, 2577-2587 (2003)
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/gene="VVA1131"
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                                                                                  /gene="VVA1134"
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                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IASVAFITHWETKKTK"
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/transI_table=11
/product="putative transporter, DME family"
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/db_xref="GI:37201334"
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/gene="VVA1130"
/note="identified by
                                                                                                                                                                                                                                                                                                                                                                       'gene="VVA1133"
                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="VVA1133"
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|
| Gene="VVA1132;
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protein_id="BAC97157.1"
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Best Local Simi
Matches 390;
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     TCCATCGTAACAAAATTCAGGAACTTGGTTTAGGTGCGATGCTTGGTAATTCGCCAAAA 146082
                                                                                                              CGCCCTACCCTTCAACGAATCTCACATGTGGTGGCCATAGGGTCACCGCTCAAAGGCGCT
                                                                                                                                                          GCACCGTCCTGTGAAACCCTCTCCCCATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCT
                                                                                                                                                                                                                                                                                                                  AATATTGATGAAGAAAAAGTTTTCCAATCCATAGACAAAGCGCTCAGCACGACGACAGGG 145902
                                                                                                                                                                                                                                                                                                                                                                       CTCAGCTTGCGCCTAAAAAATTGGGCTATCAAACAAAAACGCTCACCTACAATACAGTC
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                                                       TCCATTGTCAATAAAATTGAGCAATTAGGTTTAGGGGGGCACTAGGTAATTCAGCAGAA 1914
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nilarity 62.9%;
Conservative (
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KRLLAASFFLYALGGGCLTMAFESSYSLIAAFFRY
KRLLAASFFLYALGGGCTAVATGAGGTTVAMGCFAVLLLKKGKVMTTP
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9360. .10247
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complement (7650.
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Pred. No. 1.7e-55;
0; Mismatches 226;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                               Direct Submitseion

3 (bases 1 to 30231)

Rhee,J.H., Kim,S.Y., Chung,S.S., Lee,S.E. and Choy,H.E.

Direct Submitseion

Submitted (13-DEC-2002) Department of Microbiology, Genome Research

Center for Enteropathogenic Bacteria, Chonnam National University

Medical School, Hak-1-Dong, Dong-Gu, Kwang-Ju 501-746, South Korea

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Rhee,J.H.

Characterization and Pathogenic Significance of Vibrio vulnificus Characterization and Pathogenic Significance of Vibrio vulnificus Antigens Preferentially Expressed in Septicemic Patients Infect. Immun. 71 (10), 5461-5471 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrionaceae, Vibrio.
1 (bases 1 to 30231)
Kim, Y. R. Lee, S.E. Kim, C.M.,
Chung, S.S., Choy, H.E., Progule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio vulnificus CMCP6
Vibrio vulnificus CMCP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AE016810 AE016796
AE016810.1 GI:27358548
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Jeong, H., Moon, Y.H. and Kim, J.J.
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                                                                                                                                                                 complement (70. .1368)
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complement (70. .1368)
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                                                                                                                                                                                                                                                                                                         organism="Vibrio vulnificus CMCP6"
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FRPISQVIAIAAENSKPLALLGALRTGAIDVIATSVSNALTVLNLDEQMQGKAQ"
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/locus_tag="VV20550"
/note="contains sigma factor-related N-terminal domain;
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LHATERSWWGMGADVFINQMIELGIPSEKLVIGAAFYGRGWQGTKDYDGQAPKGDLLS
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AGVVEIGCNITANNAAVEIVMPALGGNL"
                                                                                                                                                                                                                                                                                                                       DGRIIGMTTFGESAPADQLFEMFGFTVENVVNTAKELLA"
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2966. .3916
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/db_xref="GI:27358550"
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3998. .5989
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/note="COG0021"
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note="COG0176"
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transl_table=
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301. .6864
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complement(11177, .1222
/locus_tag="VV20558"
/note="DAHP; COG0722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYLAPIRAPRIIGYVLFGFEITHQRISLASQLAGVDIALLSSLSDSSNIYVVSNEAQI
KAYFSSLAELRETASSTMQDRALADRVETTETTEKLDWQHWYYVFLESLDAASLRF
DKLASQYLWVSGLAIVLFTLAVLALSHRVIRPLITLTKATEALADGNYTATIEGTQRF
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GSDELADSVTRIKQRLDIPFYWDDFDIDISVSJGVATWPSDGGDVDSILNASQIAWYS
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SIDDFGTGYSSLGYLQRLFVNRELKVDKSFVLAWLENDRDKJTSCSTIHLAHSIGLQVV
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ATATTYQLSEQAQKVSQFMEEIGGIAEQTNLLALNAAIEAARAGEQGRGFAVVADEVR
ALSGRTSNATLQIRSSIDTMLATIQSWQNDILENKQQTESCSEVAAISAERLSEVEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="msalisnsahetilkeheqlusttdlkgvitycneafcriaefs
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sapulaomlsldgtystlanmkplttlallfroelidteqqlkkalqskepsuskliys
GKNQFSIadffikmasarirtulgrmtdsarplocladdlsatteeusgalsqaasdi
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complement (9304. .10866)
/locus_tag="VV20557"
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WKGLINDPYLNDTYKLNDGLRMGRKLLLDLTDMGLPTASEFLDMITPQYVADLISWGA
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/locus_tag="VV20557"
/note="other COG candidate exists; COG0840"
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AARVDASIAVLIDHQWALQALSEDDISEASRKELVTAIKQFSTARPYHLMIYKGKPTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGARTTESQVHRELASGLSCPVGFKNGTDGNIKIASDAIRSASASHHFLSVTKYGHSA
IVETAGNPDCHIILRGGKEPNYSAAHVSAVKEELATSGLPQKVMIDFSHANSSKQYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRSMSQLMATVAASADNQMQLSSQVNQHIHSIVTTSEQNLAATYSVEENSQKLKSRVD
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/transI_table=11
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/db_xref="GI:27358555"
                                                                                                                                                                                                                                                                                                                                                                                               TVLRQLANAVAARRAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                  QMLVADDVSEQLAAGEEAIFGVMIESHLVEGRQDLVDGKAATYGQSITDACIGWEDTE
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                           /trans]_table=11
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/db_xref="GI:27358554"
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translation="MKKLAVTLSAVLASSGFFSATANAAWSDLYFGGKIGYVNLDDAC"
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 FEATURES
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Best Local Similarity
Matches 390; Conserv
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Sequence
AX023555
                              Barth, G., Juretzek, T. and Mauersberger, S. Recombinant haploid or diploid yarrowia lipolytica cells for the functional heterologous expression of cytochrome p450 systems Patent: WO 0003008-A 10 20-JAN-2000;
                                                                                                                               synthetic construct synthetic construct
                 UNIV DRESDEN TECH (DE
                                                                                                                                                                                  AX023555.1
                                                                                                                 artificial sequences
                                                                                                                                                                                                                                                                                                                   CCAGCATTCTCACTTCAGGC 260049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGGGTTAAAAGAACACGACGAAGAATCCCGCTATCCACAAAAATCAGGCAGTATTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGCAATGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCG 1614
                                                                                                                                                                                                                                                                                                                                                   TCGTTATGACCGCTTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                  ACCACTTCATACGAGAATGCTGTTTAATCATTCCGTTGCCGAGCAAATCGACCACTTTCT
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DDIVKDMDANFFGIGITYLFGGASSAATAAAAANETAVEPRPAEEVKQEEPVAEFILL
AEEPKPEPKPEMVTKFSNQQYNQELFATGSSKLSAGGKQALTFLAEVLIKYPDAEAEI
Location/Qualifiers
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7 from Patent W00003008.
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EMBL-Datenbank X=72848"
                                                                                                                                                                                                                                                                              /note="ringf rmig geschlossene DOUBLEstr ngige DNA, Yarrowia lipolytica/Escherichia coli-DNA Plasmid p671CLpro"
                                                                                                                                                                                 4654. .5384
/note="Zeta-Element aus Retrotransposon Ylt1 aus Yarrowia
lipolytica. Schmidt-Berger et al. 1994, J Bacteriol 174,
2477-82"
                                                                                                                                                                                                                                                                  complement (16 .2151)
                                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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1. .7057
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                                                                                                           Score 226.4; DB 6;
Pred. No. 1.4e-54;
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Recombinant haploid or diploid yarrowia lipolytica cells for the functional heterologous expression of cytochrome p450 systems Patent: WO 0003008-A 6 20-JAN-2000;
UNIV DRESDEN TECH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct
synthetic construct
artificial sequences.
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Sequence 6 from Patent W00003008.
AX023551 GI:10183912
                      CTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCG 2510
                                                                                                     ATCAGAGCTTTCCCATGCAATAAACAATCCGCGACTTTACGTCTGGCCGCTTTAACTAAA 2330
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  CTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCG
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                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                 complement (2361. .4496)
/note="Promotor des ICL1-Gens
EMBL-Datenbank X=72848"
                                                                                                                                                                                                                                                                                                                                                                     /note="Terminator des ICL1-Gens aus Yarrowia lipolytica" complement (1959. .2354)
/note="Intron in ICL1-Gen aus Yarrowia lipolytica EMBL-Datenbank X=72648"
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/db_xref="taxon:32630"
/note="ringf rmig geschlossene DOUBLEstr ngige DNA,
/note="ringf rmig geschlossene DOUBLEstr ngige DNA,
Yarrowia lipolytica/Escherichia coli-DNA Plasmid p6
complement(277. 9373)
                                                                                                                                                                                                                                                                              /note="Zeta-Element aus LTR des Retrotransposon YT1 aus Yarrowia lipolytica. Schmidt-Berger et al. 1994, J Bacteriol 176,2477-82"
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Pred. No. 1.4e-54;
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from Patent WO0003008.
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Barth, G., Juretzek, T. and Mauersberger, S. Recombinant haploid or diploid yarrowia lipolytica cells for the functional heterologous expression of cytochrome p450 systems patent: WO 0003008-A 8 20-JAN-2000;
                                                                                                                                                                                                                                                                                                               CGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGA
                                                                                                                         CTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCG
                                                                                                                                                                                                              CAACACCCGCTGACGCCCCTGACGGGCTTGTCTCCCCGGCATCCGCTTACAGACAAG
                                                                                                                                                                                                                                                                            ATCAGAGCTTTCCCATGCAATAAACAATCCGCGACTTTACGTCTGGCCGCTTTAACTAAA
                                                                                    CTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCG
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lipolytica. Schmidt-Berger et al. 1994, J Bacteriol 174,
2477-82"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (3801. .5983)
/note="Promotor des ICL1-Gens aus EMBL-Datenbank X=72848"
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/note="Intron in ICL1-Gen aus Yarrowia lipolytica
EMBL-Datenbank X072848"
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EMBL-Datenbank X=72848"
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Yarrowia lipolytica/Escherichia coli-DNA Plasmid p6
complement(3. .274)
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|db_xref="taxon;32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 226.4; DB 6
Pred. No. 1.5e-54;
0; Mismatches 51
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Sequence 6 1
AR371489
AR371489.1
                                                                                                                                                                                                                                                                                           1073 bp
Sequence 6 from Patent W00151654.
AX195443
AX195443.1 GI:15385989
                                                                                                                                                                         gamples
patent:
                                                                                                                                                                                                    de Beuckeleer,M.
Methods and kits for identifying elite event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: US 6395485-A 6 28-MAY-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
1 (bases 1 to 1073)
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synthetic construct
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                                                                                                                                           WO 0151654-A 6 19-JUL-2001;
CropScience N.V. (BE)
Location/Qualifiers
                                                   /organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="sequence comprising a 5'
GAT-ZMI"
            /note="plant DNA"
286. .307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="genomic |
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/note="binding site
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from patent US 6395485.
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Pred. No. 2.9e-54;
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primer COR17"
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                                                                      flanking
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Matches 226; Conserv
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OS Artificial Sequence
PN JP 2002533126-A/11
PD 08-OCT-2002
PR 23-DEC-1999 JP 200059
PR 23-DEC-1998 IT MI 98A
PI GIUSEPPINA BESTETTI, S
ORSINI,
                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 2297)
Bestetti,G., Cali,S., Ghisotti,D., Orsini,G., Ton
Recombinant bacterial strains for the production
nucleosides and modified analogues thereof
Patent: JP 2002533126-A 11 08-OCT-2002;
                                                                                                                                                                                                                                                                               PI GIANCARLO TONON, GABRIELE ZUFFI
PC C12N15/09, C12N1/21, C12N9/10//C12P19/38, C12P19/40, C12N15/00
Description of Artificial Sequence: cloning vector derived CC
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                 TGCTCTGATGCCGCATAGTTAAGCCAGCCCGGACACCCGCCAACACCCGCTGACGCCCC
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23-DEC-1999 JP 2000591198
23-DEC-1998 IT MI 98A002792
GIUSEPPINA BESTETTI, SIMONA CALI, DANIELA GHISOTTI, GAETANO
                                                                         Conservative
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/organism='Artificial
Location/Qualifiers
1. .2297
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/note="T-DNA of pUC/Ac"
complement(466. .487)
/note="binding site of primer COR18"
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                                                                      Score 224.8; DB 6;
Pred. No. 3.4e-54;
0; Mismatches 2;
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Pred. No. 2.9e-54;
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Search completed: April 30, Job time: 10412.6 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bestetti,G., Cali,S., Orsini,G., Tonon,G., Zuffi,G. and Ghisotti,D. Recombinant bacterial strains for the production of natural nucleosides and modified analogues thereof Patent: WO 0039307-A 11 06-JUL-2000; ESSTETTI GIUSEPPINA (IT); CALI SIMONA (IT); NORPHARMA SPA (IT); ORSINI GARTANO (IT); TONON GIANCARLO (IT); ZUFFI GABRIELE (IT); GHISOTTI DANIELA (IT)
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AX027819
AX027819.1 GI:10188663
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1. .2297
                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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/noTe="cloning vector derived from pUC18"
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2578
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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Claim 14; SEQ 1D NO 41398; 1766pp; Engiten. The invention relates to an isolated nucleic acid comprising any carry for the form of the fo	WPI; 2003-029926/02. P-PSDB; ABU49658. New antisense nucleic acids, useful for homologous nucleic acids requir isolate candidate molecules for raticolate 14. SEO ID NO 41388: 1766m.	21-MAR-2001; 2001US-00815242. 06-SER-2001; 2001US-00948993. 25-CCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0072851. 06-MAR-2002; 2002US-0362699P. (ELIT-) ELITRA PHARM INC. Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	Vibrio chole WO200277183- 03-OCT-2002. 21-MAR-2002;	Prokaryotic essential gene #35185. Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.	SULT 1 A53528 standard; I ACA53528; ACA53528;

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

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CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the CC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for CC proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits proliferation; (8) CC identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC organism acts; (9) manufacturing an antibiotic; (10) profiling a CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the exent CC which each of the strains is present in a culture or collection of Strains; or (13) identifying the target of a compound that inhibits the exent CC which each of the strains is present in a culture or collection of Strains; or (13) identifying the target of a compound that inhibits the exent CC identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for cellular proliferation to island the candidate molecules for rational CC compound the cardet of the printed specification, but was obtained in the target prokaryotic essential genes. Note: The sequence data for this patent did cnot form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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88888888888888888888888888888888

Sequence 717 BP; 175 A; 165 C; 187 G; 190 T; 0 U; 0 Other;

Query Match Best Local Similarity

15.8%;

1.6e-113

DB 7; 193;

Length 717;

0

Matches

524;

Conservative

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CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense CC the polypeptide; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation of (8) identifying a gene required for cellular proliferation or the biological pathway in which hat the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC which each of the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression

Claim 14; SEQ ID NO 41399; 1766pp; English.

isolate candidate molecules for rational drug discovery programs

Ś	1387 ATCGTCAGTACCAATAAAATGGCCGCATCTTGTAAAGGCAAAGGAGCCAAACCAGCCACC 1446
皮	601 ATTGTCAGTACCAATAAAATTGCCGCCTCTAGCAAAGGTAAAGGCGGCAAACCTGCGACG 660
Ş	1447 GTTTATCGTCTTGCCAGTCATGAAGTCACCTATTTTCAAACCTGTTTACGAGGTTAA 1503
ઠ	661 GTTTATCGCTTAGCCAGTAACGAAGTCATCTATTTTCAGACTTGCTTG
RESULT	TT 2
E &	ID ACA53529 standard; DNA; 1308 BP.
88	ACA53529;
3 33	19-JUN-2003 (first entry)
183	Prokaryotic essential gene #35186.
223	Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
2 S	Vibrio cholerae.
¥ 23 \$	WO200277183-A2.
ž B ž	03-OCT-2002.
4 # \$	21-MAR-2002; 2002WO-US009107.
	21-MAR-2001; 2001US-00815242.
	06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.
	08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.
PAX	(ELIT-) ELITRA PHARM INC.
222	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW; wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
R R R	WPI; 2003-029926/02. P-PSDB; ABU49659.
7 P P	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to

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WPI; 2003-268322/26.

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RESULT 3
ABZ83659
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XX ABZ8
AC ABZ8
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XX TOX1
XX TOX1
XX TOX1
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                                                                                                                                                 16-AUG-2001;
                                                                                                                                                                                                                        16-AUG-2002; 2002WO-US026514
                                                                                                                                                                                                                                                                                                                                                                     WO2003016500-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxicologically relevant gene; toxicological response; gene;
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                                                                      (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
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   RT,
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   Adkins K,
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Pred. No. 8.
   Pickett GG,
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   Kier LD,
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consisting it is a separate to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a control of the presence of a toxic response to the agent. Also determining the presence of a toxic response to the agent. Also conscribed: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in ABS2842 ct to ABS84764, or their fragments of at least 20 nucleotides, or homologues ; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising; (a) cxposing cells to an agent or isolating the test gene expression profile of was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent, and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals
Sequence 528 BP, 124 A; 139 C; 118 G; 144 T; 0 U; 3 Other;
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                                                  TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCCGAGACGAAAAGGGCCTCGTG
                                                                                                                                                                  TACGCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCCGCCAACACCCCGCTGACGCGCCC
     ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578
                                                                                                                                           TGCTCTGATGCCGCATAGTTAAGCCAGCCCGACACCCGCCAACACCCGCTGACGCGCCC
                                                                                      TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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Pred. No. 1.4e-57;
0; Mismatches 2
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RESULT 4
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DE Gen
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DE Gen
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DE Gen
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Hun
KW cyt
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PN WC
                                                                           21-MAY-2002
                                                                                                           ABK42985 standard; DNA; 878
                                                                           (first entry)
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Genomic sequence #884 encoding novel human connective tissue polypeptide.

Human; connective cytostatic; gene; tissue related disorder;

WO200155343-A1

02-AUG-2001. 17-JAN-2001;

2001WO-US001322

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05-DEC-2000; 2000US-0256719p 06-DEC-2000; 2000US-0251479p 08-DEC-2000; 2000US-0251856P 08-DEC-2000; 2000US-0251868p 08-DEC-2000; 2000US-0251899p 08-DEC-2000; 2000US-0251999p 08-DEC-2000; 2000US-0251999p 11-DEC-2000; 2000US-0251990p 11-DEC-2000; 2000US-0259679p 11-DEC-2000; 2000US-0259679p (HUMA-) HUMAN GENOME SCI INC ROSEN CA, Barash SC, Ruben	17-NOV-2000; 2000US-0249214P 17-NOV-2000; 2000US-0249215P 17-NOV-2000; 2000US-0249217P 17-NOV-2000; 2000US-0249217P 17-NOV-2000; 2000US-0249248P 17-NOV-2000; 2000US-0249248P 17-NOV-2000; 2000US-0249249P 17-NOV-2000; 2000US-0249264P 17-NOV-2000; 2000US-0249269P 17-NOV-2000; 2000US-0249269P 17-NOV-2000; 2000US-0249269P 17-NOV-2000; 2000US-0249269P 17-NOV-2000; 2000US-0249209P 01-DEC-2000; 2000US-0250301P 01-DEC-2000; 2000US-0251030P 05-DEC-2000; 2000US-0251030P	08-NOV-2000; 2000US-0246478 08-NOV-2000; 2000US-0246479 08-NOV-2000; 2000US-0246479 08-NOV-2000; 2000US-0246524 08-NOV-2000; 2000US-0246524 08-NOV-2000; 2000US-0246526 08-NOV-2000; 2000US-0246526 08-NOV-2000; 2000US-0246630 08-NOV-2000; 2000US-0246610 08-NOV-2000; 2000US-0246610 08-NOV-2000; 2000US-0246611 08-NOV-2000; 2000US-0246611 08-NOV-2000; 2000US-0249207 17-NOV-2000; 2000US-0249209 17-NOV-2000; 2000US-0249209 17-NOV-2000; 2000US-0249211 17-NOV-2000; 2000US-0249211 17-NOV-2000; 2000US-0249211 17-NOV-2000; 2000US-0249211	PR 29-SEP-2000; 2000US-0236367P. PR 29-SEP-2000; 2000US-0236368P. PR 29-SEP-2000; 2000US-0236368P. PR 29-SEP-2000; 2000US-0236370P. PR 02-OCT-2000; 2000US-0237037P. PR 02-OCT-2000; 2000US-0237038P. PR 02-OCT-2000; 2000US-0237038P. PR 02-OCT-2000; 2000US-0237039P. PR 02-OCT-2000; 2000US-0239937P. PR 13-OCT-2000; 2000US-0239937P. PR 13-OCT-2000; 2000US-0249560P. PR 20-OCT-2000; 2000US-0241785P. PR 20-OCT-2000; 2000US-0241785P. PR 20-OCT-2000; 2000US-0241787P. PR 20-OCT-2000; 2000US-0241787P. PR 20-OCT-2000; 2000US-0241785P. PR 20-OCT-2000; 2000US-0241785P. PR 20-OCT-2000; 2000US-0241787P. PR 20-OCT-2000; 2000US-0241785P. PR 20-OCT-2000; 2000US-0241808P. PR 20-OCT-2000; 2000US-0241808P. PR 20-OCT-2000; 2000US-0241806P. PR 20-OCT-2000; 2000US-0244875P. PR 08-NOV-2000; 2000US-0246475P.

31-JAN-2000 24-FEB-2000) 24-FEB-2000) 16-APR-2000) 17-MAR-2000) 17-MAR-2000) 17-MAR-2000) 17-JUN-2000) 17-JUN-2000 17-JUN-2000 17-JUN-2000 17-JUN

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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polypucleotide (CDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polymucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but the obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1872; 673pp; English.
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 ; 2000US-0179065P.
; 2000US-0180628P.
; 2000US-0184664P.
; 2000US-0186350P.
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                                                                Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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2000US-0240960P.
2000US-0241221P.
                                                                                                                                                                                   GENOME SCI INC.
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The present : polypeptides

SEQ ID

NO 1982; 1180pp; English.

invention relates to the isolation s (AAU22915-AAU23814), and the cDNA

of novel hun and genomic

human enzyme

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 04-FEB-2000;
24-FEB-2000;
24-FEB-2000;
26-FEB-2000;
10-MAR-2000;
17-MAR-2000;
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28-JUN-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40247
                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen;
cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0199076P,
2000US-0198123P,
2000US-0205515P,
2000US-0209467P,
2000US-0215135P,
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Pred. No. 1.9
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2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 2000US-0218290P. 2000US-022964P. 2000US-0222964P. 2000US-0224518P. 2000US-0224519P. 2000US-0225214P.

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20-OCT-2000)
21-NOV-2000)
08-NOV-2000)
17-NOV-2000)
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the
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2000US-0225213P.
2000US-0225266P.
2000US-0225266P.
2000US-0225267P.
2000US-0225267P.
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2000US-0225759P.
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Matches 226; Conser-
  31 JAN-2000

04-FEB-2000;

24-FEB-2000;

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2000US-0184654P.
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2000US-0225266P.
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2000US-0240960P.
2000US-0241221P.
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                                                                                        Query Match 8.7%;
Best Local Similarity 99.1%;
Matches 226; Conservative
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01-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                     Sequence 878 BP;
                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                               Disclosure;
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             TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
                                            TGACGGGCTTGTCTGCTCCGGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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2000US-0246611P.

2000US-0246611P.
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2000US-0249207P.
2000US-0249208P.
2000US-0249209P.
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                                                                                       Score 224.8; DB 4; Length 878; Pred. No. 1.9e-57; 0; Mismatches 2; Indels 0
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XX Huma
XX Huma
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XX Homc
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17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
28-UNN-2000;
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30-UNN-2000;
11-UL-2000;
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11-AUG-2000;
11-AUG-200
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    2000US-0186350

2000US-0199074

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2000US-0199076

2000US-0214886

2000US-02166479

2000US-02166879

2000US-0216880

2000US-02174879

2000US-02174969

2000US-0224519

2000US-02252149

2000US-022522149

2000US-022522149

2000US-0225
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2000US-0180628P
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2000US-0230437P.
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2000US-0232081P.
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2000US-02333063P.
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2000US-0233064P.
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01-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
Human; foetal tissue antigen; ds; antiinflammatory; neuroprotective;
                       Human DNA for a novel foetal antigen, SEQ ID No 2106.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
                                                   17-DEC-2001
                                                                             AAS34682;
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0; Mismatches
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immunomodulator; cardiovescular, autoimmu cardiovescular, autoimmu hyperprocliferative disorder; cardiovescular disorder; cardiovescular disorder; cardiovescular disorder; cardiovescular disorder; cardiovescular disorder; cardiovescular disorder; disease; inf hold healing; epithelia healing; epithelia hold healing; e
omodulator; cardiovascular; ovascular; autoimmune disea; proliferative disorder; bre; ovascular disease; breitheris disease; breitheris disease; infection; breitheris disease; infection; breitheris disease; infection; breitheris disease; infection; cardiac infection; proliferative disease; proliferative disease
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asm; cancer; cerebrovascular disorder; sytem disorder; corneal infection; food additive.
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20000US 20000U
$\begin{array}{c} 3.3 \\$

20-NOV-2003 (first entry)

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CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g., carbbite, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a common state of the state of the antigens can also be used in diagnosing a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic communoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune complasms of the breast or liver, cardiovascular disorders e.g. cardiac complasms of the breast or liver, cardiovascular disorders e.g. cardiac complasms of the breast of the culture, hyperproliferative disorders e.g. cardiac complete can disorders e.g. Alrheimer's disease, infections caused by complete can also be used to aid wound healing and epithelial corporates, to regenerate tissues and in chemotaxis. The polypeptides can complete capabilities, for supporting cell culture of primary completes, to regenerate tissues and in chemotaxis. The polypeptides can consider the constant, minerals, cofactors and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and components in the specification. The present sequence is a genomic DNA fragment from a gene encoding a foetal antigen of the constant of the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly the printed specification.
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08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel nucleic acids encoding novel human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2106; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  excretory, gastrointestinal, reproductive, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCÎ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACGCTGATGCCGCATAGTTAAGCCAGCCCGGACACACCCCGCCAACACCCCGCTGACGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                 TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
                                              ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCCGCCAACACCCCGCTGACGCCCCC
ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG
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                                                                                                                                                    TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCGCGAGACGAAAAGGGCCTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 224.8; DB 5;
Pred. No. 1.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 10 ADA57710

ADA57710 standard; DNA; 878

X S X

ADA57710;

Sequence 878 BP; 213 A; 229 C; 199 G; 236 T; 0 U; 1 Other;

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diagnosing, treating or preventing e.g. immune disorders, or inflammatory conditions, respiratory disorders, cancers, CNS disorders, or inflammatory conditions, respiratory disorders, cancers, CNS disorders, or inflammatory conditions, respiratory disorders, cancers, CNS disorders, or inflammatory conditions or antibody fragments that bind to the polypeptides, according the polypeptides, agonists or antagonists that binds to the polypeptides are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for disposing, treating or preventing an e.g. immune compositions for conditions (e.g. inflammatory bowel disease, compirative or Crohn's disease), respiratory disorders (e.g. sathma and compositions or conditions or ischaemic brain injury), neurodegenerative disorders (e.g. parkinson's disease), and comply disorders (e.g. parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The coplymucleotides are useful for chromosome identification, chromosome comping, for controlling gene expression through triple helix formation cor antisense DNA or RNA, in gene therapy, for identifying individuals or artisense DNA or RNA, in gene therapy, for identifying individuals or probes. The polypeptides are useful for as molecular weight markers on gels, to raise antibodies, for testing biology, and as hybridization creating or preventing neural disorders, immune system disorders (c.g. abacterial artificial chromosome (BAC) fragment containing the gene encoding one of the polypeptides of the invention. Note: The sequence corresponds to a bacterial artificial chromosome (BAC) fragment containing the gene cobatained in electronic format directly from WIPO at cot abacterial artificial chromosome (BAC) fragment containing the gene obtained in electronic format directly from WIPO at
cardiovascular; antiarterioscierotic; gene therapy; human secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy; multiple sclerosis; ischaemic brain injury; Parkinson's disease; Alzheimer's disease; atheroscierosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology; ds; gene; bacterial artificial chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001;
19-JUL-2001;
13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; cerebroprotective; neuroprotective; nootropic,
cardiovascular; antiarteriosclerotic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC fragment containing human secreted protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 592 new human secreted polypeptides useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1903; 1754pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-2002; 2002WO-US008278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; antiinflammatory; antiasthmatic;
                                           ftp.wipo.int/pub/published_pct_sequences.
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2001US-0306171P.
2001US-0331287P.
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RESULT 11
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Best Local S
Matches 226
treating or ameliorating medical conditions e.g. by protein or gene therapy. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind to the polypeptide are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating cancer or other hyperproliferative disorder. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating cancer or other hyperproliferative disorders including neoplasms, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; camcer; hyperproliferative disorder; rheumatoid arthritis; autoimmune disorder; haematopoietic disorder; anaemia; allergic reaction; asthma; cardiovascular disorder; wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; vulnerary; cardiant; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 1958; 3205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing preventing or treating cancer or other hyperproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                               ADA40566-ADA41501
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                                                                                                                                                                                                                                            invention relates to novel genes ADA39629-ADA40565 and proteins
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                                                                                                                                                                                                                                                                                                                                                                                    allergies or AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
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ilarity 99.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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Pred. No. 1.9e-57;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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RESULT 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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12-JUN-2003 (first entry)

Human secreted protein BAC clone SEQ ID NO 1086

vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular di Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

Homo sapiens.

WO200295010-A2

28-NOV-2002

19-MAR-2002; 2002WO-US009785

21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA,

Disclosure; SEQ ID NO 1086; 1881pp; English.

disorders such as arrhythmia.

Novel human secreted WPI; 2003-129429/12

secreted proteins, useful for detecting, preventing, prognosticating, treating and/or ameliorating cardiovascular

agnosing,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                     Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; biliary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunosuppressive; vulnerary; chromosome 15; gene; ds.
                                                                                                                                                                                  Secreted protein gene 74 genomic fragment HJACG30, SEQ ID NO:619
                                                                                                                                                                                                                                                                                                                      ABZ71509 standard; DNA;
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Pred. No. 1.9e-57;
0; Mismatches 2
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RESULT 14 ADB91870 ID ADB91

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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99.1%;
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Pred. No. 1.9e-57;
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                                                                                                                                                                                                                                                                                                       CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-CC ADB91834. Also disclosed is a recombinant vector comprising a polynucleotide of the invention, and a recombinant bost cell comprising the recombinant vector. The polypeptide of the invention is useful in clientifying a binding partner by contacting the polypeptide with a clientifying a binding partner by contacting the polypeptide with a composition for the polypeptide. The polypeptide, polynucleotide, antibody or its fragment, agonist or antagonist are useful for preparing a pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes. The present sequence is that of the human immunoglobulin Fc portion used to generate fusion proteins, increasing the stability of the fused protein as compared to the secreted protein conly. Note: The sequence data for this patent did not form part of the grinted specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          Matches 226;
                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                     Sequence 878 BP; 213 A; 229 C; 199 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding a human secreted protein is useful in diagnosing treating diabetes or conditions related to diabetes.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; gene therapy; antidiabetic; diabetes; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated nucleic acid molecules ADB91065-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 816; 1537pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-2002; 2002WO-US008124.
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                                                                                                                                                                                                          2351 TACGCTGATGCCGCATAGTTAAGCCAGCCCCGACAACACCCGGCCAACACCCGCTGACGCGCCC
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                                                                                                                        TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCGCGAGACGAAAAGGGCCTCGTG 2530
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                                                     ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 429
                                                                                                 TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCGCGAGACGAAAAGGGCCTCGTG
                                                                                                                                                 TGACGGGCTTGTCTGCTCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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Pred. No. 1.9e-57;
0; Mismatches 2;
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KW antiafteriosclerofic; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; antiallergic; antiacterinatic; dermatological;
KW nephrotopic; virucide; fungicide; antibacterial; antiparasitic;
KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
KW argan transplant rejection; immune system disorder; Bruton's disease;
KW x-linked lymphoproliferative syndrome;
W x-linked lymphoproliferative syndrome;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular; antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
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Homo sapiens

US2003054375-A1

07-MAR-2002; 2002US-00092154. 2000US-0179065P

2000US-0198123P

2000US-0224519F. 2000US-0225213F. 2000US-0225214F.

2000US-0225758P. 2000US-0225759P.

RESULT 15 ADB61141 ID ADB61

ADB61141 standard; DNA; 878 BP

2000US-0229509P. 2000US-0229513P. 2000US-0230437P.

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Best Local Similarity
Matches 226; Conserv
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neoplasias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1872; 248pp; English.
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DB; ADB59713.
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                 ATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG
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ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG
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2000US-0250160P.
2000US-0250160P.
2000US-0250391P.
2000US-0251980P.
2000US-0251980P.
2000US-0251986P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251989P.
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2000US-0251990P.
2000US-0251990P.
2000US-0251990P.
2000US-0259879P.
2000US-0259678P.
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llarity 99.1%;
Conservative
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2000US-0249217P
2000US-0249218P
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2000US-0249297P.
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Pred. No. 1.5
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14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
20-CCT-2000
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20-CCT-2000
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Search completed: April 30, 2004, 11:04:10 Job time: 1064.2 secs

CC819923 100006J AJ568083 AJ568083

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Result
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 200000000
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 227
225.4
225.4
225.4
224.8
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Match
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2578
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10519.601 Million cell updates/sec
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 CC818374
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CC818374 100004B07
CC818523 100004L13
CC819854 100006N08
CF099977 rv37e09.y
                                                                                          Description
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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CC818374
LOCUS
DEFINITION
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                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                           Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Eukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
                                                                                                                                                                                                                                                                                                                                                                                                          CC818374 linear GSS 17-JUI 100004B07R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100004B07 R, genomic survey
   Email: ddunn@genetics.utah.edu
Plate: 0004 row: B column: 07
                                     84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                      Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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CC818374
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AJ568083
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CC817752 CC8171128 CC8171128 CC8179167 CC819808 CC819808 CC819808 CC819808 CC819808 CC819005 CC819005 CC819005 CC819005 CC819005 CC817022 CC817022

100005G21 100006K23 100006K23 100004P22 100005107 8 T. brucei 100005M06 100004M06 100006011 20006011 20006011 20006011 100003M06 100003M06 100003M06 100003M06 100003M06 100003M06

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SLC, S GSS 17-JUL-2003

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REFERENCE
AUTHORS
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ORGANISM
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Best Local
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                                                                                                           JOURNAL
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High quality sequence stop: 495.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                     Dunn, D., Doak, T., Herrick, G. and Weiss, R. Paired end reads from plasmid inserts of macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 84112, USA
                                                                                                                                                                                                            Sterkiella histriomuscorum (Oxytricha trifallax) Sterkiella histriomuscorum Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichida; Oxytrichidae; Sterkiella.
                                                                                                                                                                                                                                                                                                                                                                              CC818523 496 bp DNA linear GSS 100004L13R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100004L13 R, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XII0-Gold, T1-resistant, F-"
/clone lib="Oxytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/db_xref="taxon:94289"
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94.0%;
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Pred. No. 1.
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1.2e-58;
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VERSION
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Best Local Similarity
                                                                       TITLE
                                                                                            AUTHORS
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Email: ddunn@genetics.utah.edu
Plate: 0004 row: L column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
Class: plasmid ends
                                            Sterkiella histricmuscorum (Oxytricha trifallax)
Sterkiella histricmuscorum
Sterkiella histricmuscorum
Sterkiella histrichuscorum
Sukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichida;
Stichotrichida; Oxytrichidae; Sterkiella.

1 (bases 1 to 503)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
                                                                                                                                                                                                                       GSS.
                                                                                                                                                                                                                                                                                                   CC819854 Inear GSS 17-JUI 100006N08R Oxytricha plasmid UUGC1O library Sterkiella histriomuscorum genomic clone UUGC100006N08 R, genomic survey
                                                                                                                                                                                                                                           CC819854.1 GI:32900533
           Contact: Robert B. Weiss
                               Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAAC
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//clone="UUGG10004113"
//lab host="E. Coli strain XI10-Gold, T1-resistant, F-"
//clone lib="Oxytricha plasmid UUGC10 library"
//clone lib-"Oxytricha plasmid UUGC10 library"
//note="Vector: PMD42nv; Purified macronuclear chromosomal NNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/db_xref="taxon:94289"
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mol_type="genomic DNA"
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Indels Length

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Gaps

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2387

220 2507 160 2447 100

280

Stichotrichia,

GSS 17-JUL-2003

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RESULT 4
CF099977
                                      REFERENCE
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Matches 235
                     AUTHORS
                                                                                                    ORGANISM
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                                                                                                                                                          CF099977 308 bp mRNA linear EST 22-JUL-20 rv37e09.y1 Heterodera schachtii J2 pAMP1 v1 Heterodera schachtii CDNA 5' similar to TR:Q51617 Q51617 7.6 KD ORF. ;, mRNA sequence. CF099977 GI:33139044
                                                         Heterodera schachtii
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
1 (bases 1 to 308)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Plate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                       Heterodera schachtii
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University of Utah
Rm. 308, Biomedical
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/clone_lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
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/mal_type="genomic DNA"
/db_xref="texon:94289"
/clone="UUGC100006N08"
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Pred. No. 3.7e-58;
0; Mismatches 16;
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JOURNAL
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Query Match
Best Local Similarity
Matches 226; Conserv
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sequence.
CC818574
CC818574.1
GSS.
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100004E20R Oxytricha plasmid Uhistriomuscorum genomic clone
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The library was constructed by Claire Murphy and Dr. Makedonka
Dautova at Washington University, St. Louis
(mdautova@watson.wustl.edu). The cDNA was made by using Dynabead
oligo-dT priming (Dynal). PCR based library using a modified
protocol from the SMART PCR CDNA Synthesis Kit from Clontech.
Directionally cloned into the UDG sites of pAMP1. Heterodera
schachtii J2 were provided by Bartel Vanholme of Ghent University
Possible reversed clone: similarity on wrong strand
Seq primer: -40Rp from Gibco.
Location/Qualifiers
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington University School of Medicine
14444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
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/mol type="mxXX"
/db xref="taxon:97005"
/dev stage="J2"
/lab host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Heterodera schachtii J2 pAMP1 v1"
/note="Vector: pAMP1, Site 1: Not I; Site 2: Sal I; The
library was constructed by Claire Murphy and Dr. Makedonka
Dautova at Washington University, St. Louis
(mdautova@watson.wustl.edu). The cDNA was made by using
Dynabead oligo-dT priming (Dynal). PCR based library using
a modified protocol from the SMART PCR cDNA Synthesis Kit
from Clontech. Directionally cloned into the UDG sites of
pAMP1. Heterodera schachtii J2 were provided by Bartel
Vanholme of Ghent University (Bartel.Vanholme@rug.ac.be)."
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                             GI:32898040
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Pred. No. 4.2e-58;
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e UUGC100004E20
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ry Sterkiella
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sequence.
CC820036
CC820036.1
GSS.
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Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Plate: 0004 row: E column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 364.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B. Weiss
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Paired end reads from plasmid inserts
                                                                                                            CC820036 374 bp DNA linear GSS 17-JU 100006M24R Oxytricha plasmid UUGC1O library Sterkiella histriomuscorum genomic clone UUGC100006M24 R, genomic survey
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Fax: 801 585 7177
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/clone lib="cxytricha plasmid UUGCIO library"
/clone lib="cxytricha plasmid UUGCIO library"
/note="Vector: PWD42ny, Purified macronuclear chromosomal
/note="Vector: PWD42ny, Purified macronuclear chromosomal
/note properties were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
/pWD42 (gi 4732114 |gb |xF129072.1), a copy-number inducible
/derivative of plasmid R1. The vector was ligated with
/adaptors complementary to the insert adaptors and
/purified. The sheared, adaptored mouse DNA was annealed to
/purically-competent E. Coli XL10-Gold (Stratagene) cells
/purically-competent E. Coli XL10-Gold (Stratagene) cells
/purically-competent E. Coli XL10-Gold (Stratagene)
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/mol_type="genomic DNA"
/db_xref="taxon:94289"
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                                 GI:32900898
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Pred. No. 4.7e-58;
D; Mismatches 2
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d inserts of Oxytricha trifallax
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Matches 226;
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            sequence.
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GSS.
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Plate: 0006 row: M column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid and
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Dunn,D., Doak,T., Herr
Paired end reads from
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Sterkiella histriomuscorum
Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
                                                                                                                     CC819240 414 bp I
100005D19R Oxytricha plasmid UUGC10
histricmuscorum genomic clone UUGC10
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Fax: 801 585 7177
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igh quality sequence stop: 374.
igh quality sequence stop: 374.
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ilarity 99.1%;
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/db xref="taxon:94289"

/clone="UUGC100006M24"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/lab host="E. Coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                GI:32899308
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UUGC100005D19 R, genomic
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Matches 226; Conserv
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Plate: 0005 row: D column: 19
Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
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Eukaryota; Alveolata; Ciliophora; Spirotrichea;
Stichotrichida; Oxytrichidae; Sterkiella.
                                                            464
100002C0BR Oxytricha plasmid
histriomuscorum genomic clone
sequence.
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Fax: 801 585 7177
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Paired end reads from plasmid
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igh quality sequence stop: 414.
Location/Qualifiers
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/clone lib="Oxytricha plasmid UUGCIO library"
/note="Vector: PMD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli Xilo-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/db_xref="taxon:94289"
/clone="UUGC100005D19"
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Pred. No. 5.1e-58;
Mismatches 2;
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Eukaryota; Alveolata; Ciliophora; Spirotrichea;
Stichotrichida; Oxytrichidae; Sterkiella.
                                                                               CC817727 471 bp DNA linear GS: 100003007R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100003007 R, genomic
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Location/Qualifiers
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Plate: 0002 row: C column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah
Rm. 308, Biomedical Polymers Research
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Paired end reads from plasmid inserts
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Fax: 801 585 7177
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//lab host="E. Coli strain XI10-Gold, T1-resistant, F-"
//lab host="E. Coli strain XI10-Gold, T1-resistant, F-"
//clone lib="Oxytricha plasmid UUGC10 library"
//note="Vector: PMD42nv; Purified macronuclear chromosomal DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/db_xref="taxon:94289"
                         GI:32897014
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Pred. No. 5.4e-58;
0; Mismatches 2
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inserts of Oxytricha trifallax
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                                                                                      genomic survey
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0003 row: O column: 07
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid end=
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Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
sequence.
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GSS.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Paired end reads.from plasmid inserts
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                                                                             histriomuscorum
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ids: plasmid ends
igh quality sequence stop: 471.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PMD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gif4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/db_xref="taxon:94289"
/clone="UUGC100003007"
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                     GI:32900671
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ytricha plasmid UUGC10 1
um genomic clone rrocci
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Pred. No. 5.5e-58;
0; Mismatches 2;
                                                                           491 bp DNA i
asmid UUGC10 library
clone UUGC100006J13
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d inserts of Oxytricha trifallax
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3 R, genomic
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Eukaryota; Alveolata; Ciliophora; Spirotrichea;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Plate: 0006 row: J column: 13
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
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University of Utah
Rm. 308, Biomedical Polymers Res
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                                                              AJ568083 Antirrhinum majus library cDNA clone ze35, mRNA sequence. AJ568083
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Location/Qualifiers
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Fax: 801 585 7177
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        Antirrhinum majus (snapdragon)
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ilarity 99.1%;
Conservative
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//clome="UUGC10006413"
//lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PMD42nv; Purified macronuclear chromosomal note="Vector: PMD42nv; Purified macronuclear chromosomal polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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'db_xref="taxon:94289"
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Pred. No. 5.6e-58;
D; Mismatches 2;
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                                                                                                           Antirrhinum majus
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EST 28-JUL-2003

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Stueber, K. and Schwarz-Sommer, Z.
Antirrhinum majus EST collection
Unpublished (2003)
Contact: Stueber K
                  Email: ddunn@genetics.utah.edu
Plate: 0003 row: C column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea,
Stichotrichida, Oxytrichidae, Sterkiella.
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100003C16R Oxytricha plasmid Uhistriomuscorum genomic clone
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Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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                                                                                                                                                        Rm.
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CC817752
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                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                           University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                   Unpublished (2003)
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Paired end reads from plasmid
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                                                                                                                                                        308,
quality sequence stop: 515
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llarity 99.1%;
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                                                                                                                                                        Biomedical Polymers Research Bldg.,
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/db_xref="taxon:4151
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Pred. No. 5.7e-58;
0; Mismatches 2;
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UUGC10 library Sterkiella
e UUGC100003C16 R, genomic survey
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Matches 226; Conserv
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Sterkiella histriomiscorim
Eukaryota; Alveolata; Ciliophora; Spirotrichea;
Eukaryota; Alveolata; Ciliophora; Sterkiella.
                    Email: ddunn@genetics.utah.edu
Plate: 0002 row: D column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                             macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC817128 518 bp DNA 1
100002D21R Oxytricha plasmid UUGC10 library
histricmuscorum genomic clone UUGC100002D21
                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                         Dunn,D., Doak,T., Herrick,G. and Weiss,R. Paired end reads from plasmid inserts of
                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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High quality sequence stop: 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Cxytricha plasmid UUGC10 library"
/clone lib="Cxytricha plasmid UUGC10 library"
/note="Vector: PWD42vv; Purified macronuclear chromosomal
DNA from Cxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
cligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gil4732114 | gb | AFT129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                     USA
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/db_xref="taxon:94289"
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Email: ddunn@genetics.utah.edu
Plate: 0002 row: A column: 23
Seg primer: CAPCACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 519.
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Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 519)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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100002A23R Oxytricha
histriomuscorum genom
                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                       macronuclear chromosomes
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sterkiella histriomuscorum
                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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/db xref="texon.94289"
/clone="tutoc(10002D21"
/clone=
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richa plasmid UUGC10 library Sterkiella
genomic clone UUGC100002A23 R, genomic survey
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Pred. No. 5.8e-58;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                      Dunn,D., Doak,T., Herrick,G. and Weiss,R. Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes unpublished (2003)
Contact: Robert B. Weiss University of Utah Genome Center University, of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC817796 Inear GS: 100003X14R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100003K14 R, genomic
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Sterkiella histriomuscorum
Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
                                                                  Email: ddunn@genetics.utah.edu
plate: 0003 row: K column: 14
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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High quality sequence stop: 519.
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                               ass: plasmid ends
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/clome lib="Oxytricha plasmid UUGC10 library"
/note="Wector: PMD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gil4732114 |gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/mol type="genomic DNA"
/db xref="taxon:94289"
/clone="UUGC100092A23"
                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
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Pred. No. 5.8e-58;
0; Mismatches 2;
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Search comp Job time :	Oy 24 Db 2 Oy 25 Db 2	Oy 23 Db 24 Oy 24	ORIGIN Query Mat Best Loca Matches	FEATURES source
Search completed: April 30, 2004, 18:34:55 Job time : 7322.21 secs	2471 TGCATGTGTAGAGGTTTTCACCGTCATCACCGAAACGCGAGACGAAAGGCCTCGTG 2530	2351 TACGCTGATGCCGCATAGTTAAGCCAGCCCGGACAACCACCCGCTGACGCGCCC 2410	/db_xref="texton:94289" /db_xref="texton:94289" /dclone="UJGC10003X14" /clone="UJGC10003X14" /clone="UJGC10003X14" /clone="UJGC10003X14" /clone="UJGC10003X14" /clone=lib="Oxytricha plasmid UUGC10 library" /note="Vector: PM0427N; Purified macronuclear chromosomal DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pM042 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." Query Match 8.7%; Score 224.8; DB 29; Length 519; Best Local Similarity 99.1%; Pred. No. 5.8e-58; Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	~ LI H

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Result
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2 /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3 : /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4 : /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5 : /cgn2_6/ptodata/2/ina/backfiles1.seq:*
6 : /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-481-049-6
US-08-119-518-2
US-08-119-518-2
US-08-148-0158-2
US-08-148-0158-2
US-09-418-307-1
US-09-027-169-6
5453363-2
US-09-470-661A-32
US-09-470-661A-32
US-09-470-61A-32
US-09-042-353-393
US-08-758-417A-243
US-09-039-641-21
US-09-039-641-21
US-09-039-641-27
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US-09-039-641-27
US-09-039-641-27
US-09-039-641-37
US-09-042-492D-27
US-09-042-492D-27
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US-09-042-492D-27
US-09-042-492D-27
US-09-042-353-369
US-09-042-353-369
US-09-042-353-369
US-09-039-982A-330
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Compugen Ltd.
                                      Sequence 6, Appli
Sequence 23, Appl
Sequence 2, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 1, Appli
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Sequence 32, Appli
Sequence 33, Appli
Sequence 343, Appli
Sequence 243, Appli
Sequence 21, Appli
Sequence 27, Appli
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  Sequence
Sequence
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RESULT 2
US-09-194-285-23
US-09-194-285-23
Sequence 23, Application US/09194285
Patent No. 6355479
GENERAL INFORMATION:
APPLICANT: Webb, Susan R.
APPLICANT: Winqvist, Ola
APPLICANT: Karlsson, Lars
APPLICANT: Jackson, Michael R.
APPLICANT: Peterson, Per A.

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ATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 482

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				Query M Best Lo Matches	3-09-481- Sequence Patent N. GENERAL APPLICA- TITLE O. TITLE	r Ting	444	2444	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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TACGCCTI	GCATGTGT GCATGTGT	TGACGGGCTTGTC TGACGGGCTTGTC	TACGCTGATGCCGCATAGTTAAG 	tch al Similarity 226; Conservat	09-481-049-6/c iequence 6, Application US/09481049 atent No. 6395485 ENERAL INFORMATION: APPLICANT: DE BEUCKELEER, MARC APPLICANT: DE BEUCKELEER, MARC APPLICANT: DE BEUCKELEER, MARC APPLICANTON: MICHONS FOR ID TITLE OF INVENTION: BIOLOGICAL SAM FILE REFERENCE: 514412-2025 CURRENT APPLICATION UNMERR: US/09/ CURRENT FILING DATE: 2000-01-11 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin Ver. 2.1 BQ ID NO 6 LENCTH: 1073 TYPE: DUA ORGGNISM: Zea mays 09-481-049-6				0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
TTTTTAT	TCAGAGGT	rierciec	reccecai	8.7 99.1 cvative	Cation US/0948: ON: ON: UCKELEER, Marc UCKELEER, Marc ON: METHODS FOR ON: BIOLOGICAL S14412-2025 S14412-2025 TON NUMBER: US, ATE: 2000-01-11 NOS: 14 In Ver. 2.1		4161	4054 4054 4118 4118	88888888888888888888888888888888888888
AGGTT	TTTCAC	TGCTCCCGGCATC	AGTTAJ AGTTAJ	***	94810 arc FOR CAL S US/0 1-11		4 US-0	idadac	3 US-00-00-00-00-00-00-00-00-00-00-00-00-00
TACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG	TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG	GACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAG 	CCAGCCC CCAGCCC	Score 224.8; Pred. No. 7e-); Mismatches	049 :IDENTIFYING :SAMPLES 09/481,049	ALIGNMENTS	894	- U8-464-700-54 - U9-098-287A-9 - U9-445-649-9 - U9-068-821-17 - U9-068-821-18	9-042-492 9-039-6492 9-039-6492 9-039-6492 9-042-6982 9-042-4982 9-042-4982
ATAATGGTT	;AAACGCGCG ;AAACGCGCG	AGACAAGCT AGACAAGCT	CGACACCCGCCAACAC CGACACCCGCCAACAC	DB 4; 60; 2;	ELITE EVENT		ώμά	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
TCTTAG 257	AGACGAAAG AGACGAAAG	CGCTTACAGACAAGCTGTGACCGTCTCCGGGAG 	ACACCCGCTGACG	Length 1073; Indels 0;	NT GAT-ZM1		Sequence Sequence	sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
78	GGCCTCG GGCCTCG	TCCGGGA	GACGCGCC GACGCGCC	3; 0; Gap	N IN		ω <u>1</u> ,	9, 9, 17 18	ωωωααααατιώι 00044444
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RESULT 3
US-08-119-512-2
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; OTHER INFORMATION: engineered recombinant US-09-194-285-23
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                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,512
FILLING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT
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Best Local Similarity
Matches 226; Conserv
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Patent No. 549853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MHC Class II Antigen Presenting Systems TITLE OF INVENTION: and Methods for Activating CD4+ T Cells FILE REFERENCE: TSRI 536.1 CURRENT APPLICATION UNDEER: US/09/194,285 CURRENT FILING DATE: 1999-04-12 PRIOR APPLICATION UNDEER: PCT/US97/08697 PRIOR PILING DATE: 1997-05-22 PRIOR PILING DATE: 1997-05-22 PRIOR APPLICATION NUMBER: US 60/018,175 PRIOR PILING DATE: 1996-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
EQ ID NO 23
LENGTH: 2580
                            ATTORNEY/AGENT INFORMATION:
NAMMS: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HUI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Jarrel
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ORGANISM: Artificial Sequence
INFORMATION FOR SEQ ID NO:
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           TELEPHONE: (C-
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ZIP: 02109
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227-5941
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INTRON MEDIATED RECOMBINANT TECHNIQUES
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Pred. No. 1.2e-59;
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US-08-488-015B-2
; Sequence 2, Application
; Patent No. 5780272
; GENERAL INFORMATION:
; APPLICANT: Jarrell
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Best Local Similarity
Matches 226; Conserv
                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER
COMPUTER: FOR COMPUTER
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION UNMERE: US/08/488,015B
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LOCATION: 2448..2657
OTHER INFORMATION: /pr
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OTHER INFORMATION: /product= "intron sequence"
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LOCATION: 2390..2447
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LOCATION: 2815..2890
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LOCATION: 2667..2814
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HU
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STREET: One Post Office Square
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INTRON-MEDIATED RECOMBINANT TECHNIQUES
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Pred. No. 1.3e-59;
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TELECOMMUNICATION INFORMATION:

TELEPHONE:

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US-08-814-412-17
; Sequence 17, A)
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Best Local
                                                                                                                                                                                                                                                                             PALENT NO. 6150141
GENERAL INFORMATION:
APPLICANT: Jarrell Ph.D., Kevin A.
APPLICANTION: Intron-Mediated Techniques and Reagents
NUMBER OF SEQUENCES: 46
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,412
FILING DATE: 11-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (617) 832-7000: (INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2939 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 2390..2447
OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2815..2890
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2667..2814
OTHER INFORMATION: /product= "b-globin exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 2448..2657
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2939 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: both
                                                                                                                                                                         COUNTRY: UZIP: 02109
                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 2667..2814
                                                                                                                                                                                                                                         ADDRESSEE: Choate, Hall & STREET: 53 State Street
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                                                                                                                                                                                          USA
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2815..2890
: US/08/814,412
: 11-MAR-1997
ON: 435
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Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3e-59;
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US-08-814-412-17
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Best Local Similarity
Matches 226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07415307A Patent No. 5344757
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 36
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC/DOS
SOTTWARE: WOOTSPETCH
CURRENT APPLICATION NUMBER: US/07/415,307A
FILING DATE: 19900109
CLASSIFICATION DATA:
APPLICATION UMBER: PCT/EP89/0026
FILING DATE: 12-dan-1989
FILING DATE: 12-dan-1989
FILING DATE: 12-dan-1989
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Scholer, Hans
APPLICANT: Scholer, Hans
APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for the Detection of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "plasmid DNA"
IMMEDIATE SOURCE:
CLONE: BGINV
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617 248 5000
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                                                                                                                                                                                                                                                                                  STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jarrell Ph.D., Brenda H. REGISTRATION NUMBER: 39,223 REFERENCE/DOCKET NUMBER: 00795
                                                                                                                                                                                                                                                ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2411 TGACGGGCTTGCTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holtke, Hans Joachim
Seibl, Rudolf
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  DE 38 00 642.1
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Pred. No. 1.3e-59;
0; Mismatches 2;
                                                                                                                                                                                                             360 kb
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RESULT 7
US-08-371-320-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7%;
Best Local Similarity 99.1%;
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC/DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,320
FILING DATE: 11-JAN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/415,307
FILING DATE: 09-JAN-1990
APPLICATION NUMBER: PCT/EP89/0026
FILING DATE: 12-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Holtke, Hans Joachim
APPLICANT: Seibl, Rudolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 212-688-9200
TELEPAX: 212-938-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3104 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. 5344757man D.
REJISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schmitz, Gudrun
APPLICANT: Scholer, Hans
APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for the Detection of Nucleic Acids
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-Jan-1988
APPLICATION NUMBER: DE 38 13
FILING DATE: 20-Apr-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3104 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                       CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                  E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                     USA
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Pred. No. 1.4e-59;
                                                                                                                                                                                                                                                         360 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09027169
Patent No. 6420524
GENERAL INFORMATION:
APPLICANT: CRAIG, NANCY L
TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS
                                                                                                                                     ZIP: 27608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,169

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.7%;
Best Local Similarity 99.1%;
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEFAX: 919 881 3175 INFORMATION FOR SEQ ID NO:
                                 NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 570
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 5702888man D. REGISTRATION NUMBER: 30,946
REGERENCE/DOCKET NUMBER: BOER 7:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE 38 00 642.1 FILLING DATE: 12-Jan-1988 APPLICATION NUMBER: DE 38 13 278.8 FILLING DATE: 20-Apr-1988 ATTORNEY/AGENT INFORMATION: NAME: Hanson, No. 5702888man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Anne Brown (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 300
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2378
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pred. No. 1.4e-59;
0; Mismatches 2;
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RESULT 9
5453363-2
;Patent No. 5453363
;Patent No. 5453363
; Patent No. 5453363
; Patent No. 5453363
; Patent Op Invention: PROCESS FOR THE ACTIVATION OF T-PA OR TITLE OP INVENTIC EXPRESSION IN PROXARYOTES
;ING AFTER GENETIC EXPRESSION IN PROXARYOTES
;UNMBER OF SEQUENCES: 4
;UNMBER OF SEQUENCES: 4
;UNMBER OF SEQUENCES: 4
;PAPLICATION NUMBER: US/08/206,044
;ILING DATE: 02-MAR-1994
;PRIOR APPLICATION DATA: 4
;PAPLICATION NUMBER: 942,370
;PILING DATE: 09-SEP-1992
;APPLICATION NUMBER: 498,500
;PILING DATE: 23-MAR-1990
;PILING DATE: 23-MAR-1990
;PILING DATE: 23-MAR-1990
;PAPLICATION NUMBER: 76,207
;PILING DATE: 23-MAR-1996
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Best Local Similarity 99.1%;
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "pRM2 (target plasmid)"
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les 226; Conserv
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ATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 1406
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Pred. No. 1.4e-59;
0; Mismatches 2
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RESULT

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FEATURE:

NAME/KEY: misc feature

LOCATION: (1118)..(1125)

OTHER INFORMATION: N stands for the control of the 
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, JON A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
APPLICANT: LUKE, Catherine J.
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOI
FILE REFERENCE: 454312-2440.1
CURRENT FILING DATE: 1996-10-15
PRIOR APPLICATION NUMBER: US/09/173,053
CURRENT FILING DATE: 1996-10-15
PRIOR APPLICATION NUMBER: 08/663,998
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Sequence 32, Application US/09470661A
Patent No. 6500662
GENERAL INFORMATION:
APPLICANT: Pfizer Products Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-173-053-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09173053 Patent No. 6451769 GENERAL INFORMATION:
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TITLE OF INVENTION: AN INFECTIOUS CDNA CLONE OF NORTH AMERICAN PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS) VIRUS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC10278A
CURRENT APPLICATION NUMBER: US/09/470,661A
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 3796
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Best Local Similarity 99.1%;
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                         ORGANISM: Borrelia burgdorferi
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ORGANISM: Plasmid
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Pred. No. 1.5e-59;
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US-09-042-353-393/c
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Patent No. 6255458
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Best Local Similarity
Matches 226; Conserv
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ETILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
115 07/900 860
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APPLICANT: Kay, Robert M.
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human
TITLE OF INVENTION: Producing Heterologous Antil
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                   APPLICATION NUMBER: US 08/155,301 PILING DATE: 18-NOV-1993 PRIOR APPLICATION DATA:
                                                                                             FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                        APPLICATION NUMBER: US 07/990,860 FILING DATE: 16-DEC-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/053,131 FILING DATE: 26-APR-1993 PRIOR APPLICATION DATA:
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FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                APPLICATION NUMBER:
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03-DEC-1993
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                     US 08/161,739
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Pred. No. 1.5e-59;
0; Mismatches 2;
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RESULT 13
US-08-758-417A-243/c
US-08-758-417A-243/c
; Sequence 243, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT Lomberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals
Producing Heterologous Antibodies
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-042-353-393
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TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGIH: 3819 base pairs
TYPE: nucleic acid
cypanterners . . . . . . . . . . .
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Best Local Similarity
Matches 226; Conserv
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APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 08/758,417
PRIOR APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
APPLICATION NUMBER: WO PCT/US97/21803
PRIOR APPLICATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
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FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
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FILING DATE: 07-DEC-
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 014
TELECOMMUNICATION INFORMATION:
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10-OCT-1995
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Pred. No. 1.5e-59;
0; Mismatches 2
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NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

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; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243
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Best Local Similarity 99.1%;
Matches 226; Conservative 0
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                            TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCCGGGAGC
ATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 1938
                                           ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578
                                                                                                                                 TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG 2530
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                      TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG
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APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
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FILING DATE: 10-CCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
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FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
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TELEFAX: (415) 576-0300
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STATE: California
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Pred. No. 1.5e-59;
0; Mismatches 2
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RESULT 14

GENERAL INFOR

INFORMATION:

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APPLICANT:

Sprent, Jonathan

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RESULT 15
US-09-039-641-21
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NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEPAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3875 base pairs
Sequence 21, Application US/09039641 Patent No. 6251627
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Patent No. 6225042
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,982A
FILING DATE: 16-MAR-1998
CLASSITICATION: 435
CLASSITICATION: 435
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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CITY: Chicago
CITY: Illinois
TTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                            1662
                                                                                                                                     2531 ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578
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20 No. 6225042th Wacker Drive,
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ilarity 99.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 224.8; DB 3;
Pred. No. 1.6e-59;
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COUNTEX:

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/039,641

FILING DATE: 8-MAR-1995

CLASSIFICATION NUMBER: US/09/039,641

FILING DATE: 8-MAR-1995

CLASSIFICATION NUMBER: TSRI4710

REFISHENCE/DOCKET NUMBER: TSRI4710

TELEPHONE: (312) 580-1180

TELEPHONE: (312) 580-1180

TELEPHONE: 3875 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-09-039-641-21

R.7%; Score 224.8; DB 3;
Search completed: April 30, 2004, 18:42:53 Job time : 307.986 secs
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Best Local Similarity 99.1%;
Matches 226; Conservative
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APPLICANT: Jackson, Michael
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
TITLE OF INVENTION: ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6251627th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
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                                                                                        ATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 1709
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Pred. No. 1.6e-59;
0; Mismatches 2;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Published Applications NA:*

1: /cgn2=6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2=6/ptodata/2/pubpna/US06 NEW PUB.seq:*

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16: /cgn2=6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

17: /cgn2=6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

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19: /cgn2=6/ptodata/2/pubpna/US108 PUBCOMB.seq:*
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10195.950 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	ВВ	ID	Description
1	2578	100.0	2578	16	US-10-603-260-1	Sequence 1, Appli
N	798	31.0	798	16	US-10-603-260-2	2
w	555	21.5	555	16	US-10-603-260-4	Sequence 4, Appli
4	408.2	15.8	717	13	US-10-282-122A-41398	413
ი 5	249.2	9.7	1308	13	US-10-282-122A-41399	
ი	224.8	8.7	878	യ	US-09-764-847-1872	Sequence 1872, Ap
7	224.8	8.7	878	10	US-09-764-891-10029	Sequence 10029, A
89	224.8	8.7	878	10	US-09-764-891-10033	Sequence 10033, .
9	224.8	8.7	878	13	US-09-973-278-674	Sequence 674, App
10	224.8	8.7	878	15	US-10-092-154-1872	1872
c 11	224.8	8.7	1073	ω	US-09-758-987-6	Sequence 6, Appli
12	224.8	8.7	2297	10	US-09-891-865A-11	Sequence 11, App
c 13	224.8	8.7	2462	15	US-10-365-062-5	Sequence 5, Appl
c 14	224.8	8.7	2762	15	US-10-244-142A-2	Sequence 2, Appl:

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1	-10-105-678A-	US-10-105-504A-27	US-10-105-200A-27	-10-266-463A-2	L	US-10-105-504A-21	-10-105-200A-	US-10-014-099F-14	US-10-241-332-32			US-10-258-482-3	L	-10-128	US-10-128-590-22	US-10-382-361-2	US-09-891-865A-1	US-09-891-865A-3	US-10-343-303-7	-108-	US-10-024-809-6	-09-89	-10-128-578B-	US-10-128-587A-9	US-10-128-590-9	US-09-891-865A-12	US-10-128-578B-62	-10-128-587A-6	8-590-6	
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ALIGNMENTS

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181 GATTTCAATTTGCCGATCGGGTTGAAAATGGAAAATGGCTAAATGACTGTAAAAAAGTACG 240	121 TCGCCACGTACCTTGAATGGCGATACGCAGCTGGCGTTTGCCCTTTGCTTGAGGATCCC 180	121 TCGCCACGTACCTTGAATGGCGATACGCAGCTGGCGTTTGCCCTCTTGCTTG	61 GCGGCGGCTACTTACAGAGATTAAGGCCATGACTAGCGTTTCATATAAAAATGGTGTC 120	61 GCGGCGGCTACGTTCAGAGAGTTAAGGCCATGACTAGCGTTTCATATAAAATGGTGTC 120	1 AGCTTGCACTTTATCAGCCAATACTTGCATCGGTAACTCGGCGGGCACTTGTGCCCAGTG 60	1 AGCTTGCACTTTATCAGCCAATACTTGCATCGGTAACTCGGGCGGG	Hatches 2578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%;	; ORGANISM: Vibrio metschnikovii RH530 US-10-603-260-1	TYPE: DNA	SEQ ID NO 1 LENGTH: 2578	KopatentIn :	••	CURRENT REFLICATION NUMBER: 00/10/00/200	FERENCE:	INVENTION: nucleotide	TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and a	ADDITION: OI OTTOTATION	1.cation No. US20040009570A1	Sequence 1, Application US/10603260	US-10-603-260-1	년 1

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ACATCCGTGGTACTATTTCATTAGAAAAAGAGTTTTTAGTGGCGGATATTATTGATGCC 1	1201 TTTGATCATGTCGCGCAAAITCAGCATGCGTGGCAAAAITACGCGGTTGCGGTTGAATAC 1260 	1141 CCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAATGCCGCTGGCT 1200	1081 TCCCATTACGCTTTATTAAACCCGTGGAATGTCAAACAAA	1021 AGCGATCCGCTGGTTGATGGCAACCCCAAACGCGATCCGAATGGTTGAGTGTCAGTATT 1080	961 TTTGATGCAGCGAGACGTATTTGTCGGCAAAAAGTCCATACTTATCCTAATTTTATC 1020 	901 GGCGGGATAGTGTATGACGAAGATATGACCGCTCATGGTGGAGAACCTGTCGATGAGGAT 960	841 GTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGTAAATGGGCATTGCCT 900	781 GCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTTGCGCCGAAATCTATCCAG 840	721 TATITTACATTTGACCATCATGCACTTACCTAAAATAAGCCCGTTGTTTATTAGGGAA 780 721 TATITTACATTTGACCATCATGCACTTACCTAAAATAAGCCCGTTGTTTATTAGGGAA 780	661 CGTAGTCATAACAATTACAGTACTCTTGTTATCTGAGTTATGTTTGTCACAAAGTCT 720	601 GACAAACCTAGTCAGTCGTTATTTGGCCTTATTATAATTATGGATATTGAGGGTAAGGA 660	541 CAACGTGTTGCTAACTTTGGGCGAACATAAAGTACCCTTGTAAGTTTGCAACTTTTGT 600	481 GCGATCGCTCATGATGATGACCATCCTTTCGTTCGGTTTCAGTCAG	421 CATATTGATTTTATAGGCATCAAGATCCAATAAACTGCGGATAAAAAGAGGAGAAAATAG 480	361 GCGCACAATCAATTCATAGCGCACCTCAACATCCGGATACCAACGAATGAACGGCCTGCAT 420 	301 AGCCAACTGATTGATTTCTTGGCGTACTACTCTCTAATAAATCGCTAATGATCTTCATCACT 360	41 ATTCAAATGAGGTGCATGCTGCTCTAAATAACAATGTCGGCATCCGAAAAAGCGCAATGA	181 GATTTCAATTTGCCGATCGGGTTGAAAATGGGAAATAGCGTAATGACTGTAAAAAAGGTACG 240
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CURRENT APPLICATION NUMBER: US/10/803,260
CURRENT FILING DATE: 2003-06-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: KOPAtentIn 1.71
SEQ ID NO 2
LENGTH: 798
TYPE: DNA
ORGANISM: Vibrio metschnikovii RH530
FEATURE:
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; OTHER INFORMATION: vall1 gene
US-10-603-260-2
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Best Local Similarity
Matches 798; Conserv
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Publication No. US20040009570A1
GENERAL INFORMATION:
APPLICANT: CJ Corporation
TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and
TITLE OF INVENTION: nucleotide sequence encoding the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
  1183
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GAAGAAATGCCGCTGGCTTTTGATCATGTCGCGCAAATTCAGCATGCGTGGCAAAAATTA
                                                  GAAGATTTIGGTATCGACCCCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAA 1182
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                          GAAGATTTTGGTATCGACCCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAA
                                                                                                                                                        ACTTATCCTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACGCGATCCGAAT
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                                                                                                           GAACCTGTCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCAT
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Sequence 4, Application US/10603260

Publication No. US20040009570A1

GENERAL INFORMATION:

APPLICANT: CJ COPPORATION:

TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and a TITLE OF INVENTION: nucleotide sequence encoding the same FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/603,260

CURRENT FILING DATE: 2003-06-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4

SEQ ID NO 4

ORGANISM: Vibrio metschnikovii RH530

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(555)

OTHER INDRAMATION: vall2 gene

US-10-603-260-4
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US-10-603-260-4
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Best Local Similarity
Matches 555; Conserv
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; TYPE: DNA
; ORGANISM: Vibrio
US-10-282-122A-41398
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US-10-282-122A-41398
                                                                                                                                            Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41398
LENGTH: 717
                   Query Match
Best Local Similarity
Matches 524; Conserv
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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Zyskind, Judith
Wall, Daniel
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Malone, Cheryl
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                   Score 408.2; DB 13;
Pred. No. 5.2e-113;
0; Mismatches 193;
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                     Indels
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US-10-282-122A-41399/c

US-10-282-122A-41399/ Application US/10282122A

; Publication No. US20040029129A1
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Yamamoto, Robert
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; ORGANISM: Vibrio
US-10-282-122A-41399
                                                                                  Sequence 1872, Application US/09764847 Patent No. US20020132767A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTMARE: Patentin version 3.1
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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US-09-764-891-10029
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; LOCATION: (741)
; OTHER INFORMATION:
US-09-764-847-1872
                                                                                                                                                                                                                                                             US-09-764-891-10029
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NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10029
LENGTH: 878
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                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 226; Conserv
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NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1872
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NAME/KEY: SITE
LOCATION: (741)
OTHER INFORMATION: 1
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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                      TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCGCGAGACGAAAAGGGCCTCGTG
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ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578

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APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P2
CURRENT APPLICATION NUMBER: US/09/973,278
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 60/239,899
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/227,357
PRIOR APPLICATION NUMBER: 09/227,357
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/051,926
PRIOR APPLICATION NUMBER: 60/052,793
PRIOR FILING DATE: 1997-07-08
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US-09-764-891-10033
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; NAME/KEY: SITE
; LOCATION: (741)
; OTHER INFORMATION: n equals a,t,g,
US-09-764-891-10033
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 674, Application US/09973278 Publication No. US20040044191A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 226; Conserv
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ORGANISM: Homo sapiens
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                                              APPLICATION NUMBER: 60/051,925
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: 1997-07-08
NUMBER: 60/051,929
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Pred. No. 5e-57;
0; Mismatches 2;
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 674
LENGTH: 878
LENGTH: 878
TYPE: DNA
CRCANISM: Homo sapiens
FEATURE:
PEATURE: (741)...(741)
COTHER INFORMATION: n equ
US-09-973-278-674
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PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/055,722
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,723
PRIOR APPLICATION NUMBER: 60/055,723
PRIOR PILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
                                   Best Local Similarity 99.1 Matches 226; Conservative
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Best Local
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PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/051,930
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PRIOR APPLICATION NUMBER: 60/051,918
PRIOR FILING DATE: 1997-07-08
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NUMBER OF SEQ ID NOS: 947
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PRIOR APPLICATION NUMBER: 60/058,664
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PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/058,785
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2351 TACGCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCC 2410
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                                                        Score 224.8; DB
Pred. No. 5e-57;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PCOOSCI
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 878
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US-10-092-154-1872
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                                                                                                                                                                                 Sequence 6, Application US/09758987
Patent No. US20010029014A1
GENERAL INFORMATION:
APPLICANT: De Beuckeleer, Marc
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Best Local Similarity 99.1%;
Matches 226; Conservative
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Publication No. US20030054375A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (741)
TITLE OF INVENTION: Methods and kits for TITLE OF INVENTION: samples FILE REFERENCE: 514412-2025.1 CURRENT APPLICATION NUMBER: US/09/758,987 CURRENT FILING DATE: 2001-01-11 PRIOR APPLICATION NUMBER: 09/481,049 PRIOR FILING DATE: 2000-01-11
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Pred. No. 5e-57;
0; Mismatches 2;
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                                                                                                                                                             for identifying elite event GAT-ZM1 in
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Publication No. US20030059870A1
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of TITLE OF INVENTION: natural nucleosides and modified analogues thereof FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,865A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: M198A002792
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
IENUTAL 2007
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US-09-891-865A-11
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SOFTWARE: PatentIn version 3.0

SEQ ID NO 6

LENGTH: 1073

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1073)
OTHER INFORMATION: Sequence comprising a 5' flanking region of GAT-ZM1
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Best Local Similarity 99.1%;
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Best Local Similarity
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                                                                TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTG 2530
                                                                                                                                                                      TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC
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Pred. No. 5.8e-57;
"" wismatches 2;
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192

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ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAG 2578

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APPLICANT: Ge, Yigong
APPLICANT: White, Sarah
APPLICANT: GeneSoft, Inc.
TITLE OF INVENTION: Methods of Treating Infection by Drug Resistant
TITLE OF INVENTION: Bacteria
FILE REFERENCE: 020891-00910US
CURRENT FILING DATE: 2002-09-12
FRIOR APPLICATION NUMBER: US/10/244,142A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/322,704
PRIOR APPLICATION NUMBER: US 60/322,704
PRIOR APPLICATION NUMBER: US 50/322,704
PRIOR FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver
SEQ ID NOS: 20
LENGTON
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CURRENT APPLICATION NUMBER: US/10/365,062
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 09/496,445
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: US 60/118,478
PRIOR FILING DATE: 1999-02-03
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 2462
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US-10-365-062-5/c
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US-10-244-142A-2/c
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; ORGANISM: Escherichia coli
US-10-365-062-5
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Publication No. US20030145343A1
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Best Local S
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APPLICANT: McNeish, i
APPLICANT: Ahlijanian
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APPLICANT: Ahlijanian, Michael K.
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HUMAN
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Pred. No. 1.1e-56;
0; Mismatches 2
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GENERAL INFORMATION:

APPLICANT: Moser, Heinz E.
APPLICANT: Baird, Eldon E.
APPLICANT: Buerli, Roland W.
APPLICANT: Ge, Yigong
APPLICANT: White, Sarah
APPLICANT: GeneSoft, Inc.
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TITLE OF INVENTION: Bacteria
FILE REFERENCE: 020891-09910US
CURRENT APPLICATION NUMBER: US/10/244,142A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/322,704
PRIOR FILING DATE: 2001-09-13
RUMBER OF SEC ID NOS: 20
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 2803
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Best Local Similarity 99.1%;
Matches 226; Conservative
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Best Local Similarity 99.1%;
Matches 226; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:double stranded
OTHER INFORMATION: circular Plasmid A
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Pred. No. 1.2e-56;
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Search completed: April 30, 2004, 23:19:29
Job time: 1149.07 secs

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Database :
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Listing first 45 summaries
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10745.552 Million cell updates/sec
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SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS	ON OFFICE	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AE004352/c	RESULT 1
<pre>1 (bases 1 to 10977) Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,B.K., Peterson,J.D., Umayam,L.,</pre>	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.	Vibrio cholerae Ol biovar eltor str. N16961		AE004352.1 GI:9657475	AE004352 AE003853	9 of 93 of the complete chromosome.	Vibrio cholerae O1 biovar eltor str. N16961 chromosome II, section	AE004352 10977 bp DNA linear BCT 10-OCT-2003		

gene	gene	CDS	qene	gene	JOURNAL FEATURES Source	TITLE JOURNAL MEDLINE PUMED REFERENCE AUTHORS
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Liu,Y.M., Chen,H.J., Shen,A.B., Li,J.C., Su,T.L.,
Lee,C.T., Hor,L.I. and Tsai,S.F.
Comparative Genome Analysis of Vibrio vulnificus,
Genome Res. 13, 2577-2587 (2003)
2 (bases 1 to 24190)
Chen,C.Y., Wu,K.M. and Tsai,S.F.
Direct Submission
                                                                                                                                                                                                                                                                                                                   Submitted (29-MAY-2002) Shih Feng Tsai, National Health Research Institutes, Division of Molecular and Genomic Medicine; 128, Yen-Chiu-Yuan Road, Sec 2, Taipei, Taiwan 115, Republic of China (E-mail:petsai@nhri.org.tw, Tel:886-2-8146-1041, Fax:886-2-2789-0484)
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Vibrio vulnificus YJ016
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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YJ016 DNA,
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LSSLEHASTENLSSSIDLLMLERHEKDYLARREKYLTSFDATYSQLQORIDHLSDVL
ASESIAIDDORQQIVTTLSQYQTQFHQLAAQLANIDALOSELFAARSMLKTINVLSAND
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VVLLSSLLYVIGRSILSRIKAINLLMDDIANGSGDLTVRWNAKGSDELAQLSRSFDLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="identified by GeneMark and Glimmer2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _table=11
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SEDQIGRAIGTRVGGSUHKSYLOGGERWANNAEVTANGKIETRGLISRTVIPVELD
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TGYLMWPFVKAYLTNIVEISVITLTLLVVSGLLVYRGSEDLFRPIERDGYNNTIGMLY
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| /gene="VV1713"
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| /transT table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10173. .11678)
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raliperekotgyktadekyladorsuleyfbaladdnotterkadeksdeskelgengtynkeldlavlefegdoklfn
raliperekotstekter professferent beforeten betateten be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             component"
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/db_xref="GI:37198641"
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/db_xref="GI:37198643"
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                                                                                   AAGGGAGGCAAACCCGCTCAGGTCTATAGCTTAGCGGATAAACACGTAACCTATTTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAAAGGGCTGGAAGTTCTGCTGATTAAGCGCACCAATCCTGAGAGACCACAGCATGGC 201558
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ilgqwlicffvlvsmmygalqssdrraletaltlgvslprlsatmiwetrfplwaati
tgfsrlvtevgcsmmvganimgltrniptaismeshkgafaqgvalgivlltlalvln
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Submitted (13-DEC-2002) Genotech Corp., 461-6, Jeonmin-dong, Submitted (13-DEC-2002) Genotech Corp., 461-6, Jeonmin-dong, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-DEC-2002) Department of Microbiology, Genome Research Center for Enteropathogenic Bacteria, Chomnam National University Medical School, Hak-1-Dong, Dong-Gu, Kwang-Ju 501-746, South Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuseong-gu, Daejeon 305-811, South Korea 3 (bases 1 to 306147)
Rhee, J.H., Kim, S.Y., Chung, S.S., Lee, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 306147)

Kim, Y.R., Lee, S.E., Kim, C.M., Kim, S.Y., Shin, E.K., Shir Chung, S.S., Choy, H.E., Progulske-Fox, A., Hillman, J.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterization and Pathogenic Significance of Vibrio vulnificus Antigens Preferentially Expressed in Septicemic Patients Infect. Immun. 71 (10), 5461-5471 (2003)
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Vibrio vulnificus CMCP6
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                                RVVKNVNQAKTPLMMQEKLRRCGIRSIDPVVDITNFYLLEQGOPMHAFDLAKIDGGI
VVRLAEQGEKITLLDGSEAELNADTI.VVADHNKALAIAGIFGEESGYTSETKOVLLE
CAFFAPDHIRGRARSYGHTDSSMRFEERGVDZHALQVAJARTALLVEICGGEVAPVL
AVESEAELPKENKVALRRTKLDNLLGHHIADSDVVEILERLGMTVETTAEGWVAVAPT
WRFDIAIEQDLVEEVGRIYGYDNIPNQNFAAALKMHDHQEANIPLKRVRDLLVDRGYH
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DLTSNRADCTSIRGMAREVGTURRADVTEPSVAPVAFSIDDTVAIEVKAPARGRYLG
ULTSNRADCTSIRGMAREVGTURRADVTEPSVAPVAFSIDDTVAIEVKAPARGRYLG
THE TOTAL TO
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/strain="CMCP6"
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Handfield,M.
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                                                                                                                                        complement (7347. .8123)
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complement (7347. .8123)
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EIEWSAINRKVIPEAVALSKFPANRRDIAVVVDEAVASGDIVNACLEVGGEFLKAAKL
FDVYVGKGVEEGKKSLAIAITLQSNERTLEDADIAGAVDAIVTHVSEKFGASLRD"
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db_xref="GI:27361842"
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table=
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244 CCTGTCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCATACT 303
                                                                                                                                                                                                                                                                            124 CCGAAATCTATCCAGGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                   ATGTĠĠTĊTAŤTĊĊĠĠĠĄĠĠĄŢŤŢĠŤĠŤŢŤĠĂĄĊĄĊĠĄŤŢŤĄŢĊĊĊĄĄĠĄĠĠĄĠĠĄĠĄ
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                                                                                                                                                                                                                      GAGAAAGGGCTGGAAGTTCTGCTGATTAAGCGCACCAATCCTGAGAGACCACAGCATGGC
                                                                                                                                                                                                                                                                                                                                            TTGATATTTAAGAGTTGCCGTATGATTGTTACGATTGACATGATTTGCCTGAAGCTAGGT
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Ekklhdylpdsfgesdlgissalmsqvhhgfatedddalmqraveammeshapythnl
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EMAGPFSVTQEEIHLFAGMYTRLYQDIADEHHPKIAKQGLSRFSEEVYVIENDK"
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SETRSLNDVELATIKRLRSHSKDLYQQAWQPYLTTHLEAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (11675. .11812)
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KISHLACTQSTLEALNPDIPVSYLSL"
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FDGMSDALEQPQTQLRLFGKPDINGRRRLGVVLTRRSSTEKAVDAAIESAKKIKIIY"
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AGVKSQQRAKQKIALELNNQPERITDLARATIVADDVASLVSAYEALERETRIVKVKN
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complement(10400
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[_table=11
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AUTHORS
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AUTHORS
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MEDLINE
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                                                                                                                                                                                                             Makino, K., Oshima, K., Kurokawa, K., Tagomori, K., Iijima, Y., Najima, M., Kubota, Y., Kimura, S., Yasunaga, T., Hattori, M. and Iida, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio parahaemolyticus
Vibrio parahaemolyticus
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP005085 303450
Vibrio parahaemolyticus DNA,
AP005085 BA000032
AP005085.1 GI:28808465
      Direct Submission Submitted (09-APR
                                        Oshima, K., Kurokawa, K.,
Honda, T., Shinagawa, H.,
                                                                                                                                                Genome sequence of Vibrio parahaemolyticus: a distinct from that of V cholerae Lancet 361 (9359), 743-749 (2003)
                                                                                                                                                                                                                                                                                                                                                                                  Nasu, H., Iida, T., Sugahara, T., Yamaichi, Y., Park, K.S., Yokoyama, K., Makino, K., Shinagawa, H. and Honda, T. A filamentous phage associated with recent pandemic Vibrio parahaemolyticus O3:K6 strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrionaceae; Vibrio.
                                                                                                            .2620739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCCTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACGCGATCCGAATGGT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATCATTCACGCCTACGCCAAGTTTGGTGTGGATGTGAACCGCATGACGATCAAGCGA
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                                                                                   (bases 1 to 303450)
      (09-APR-2002)
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  Ken Kurokawa, Osaka University, Genome
                                             Makino, K., Yokoyama, K., Hattori, M. and Iida, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp DNA chromosome 2,
                                                                                                                                                                                                                                 Yokoyama, K., Uda, T.,
Nakano, M., Yamashita, A.,
Honda, T., Shinagawa, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                           pathogenic mechanism
                                                                 Yasunaga, T.,
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This clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:Ken@gen-info.osaka-u.ac.jp, URLi.http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastroenteritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone was isolated from
                                                                                                                                                /trānslation="mkiehvaiwterleelkgpyekyfnavsndkyhnpkkhfssyfl
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IAKSFIATRYDADKIAVEVLPLKNYVPSDEEHQDRLTRFPNDYCHIPLDLLHKYKNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNLKAVPKALLYTLLASSLPISSVAYAAPNANESSLVQQQWEGN WFTQNEAEKLVQELYYQRAISAYYQNQPAMNYIGMRDGSESKFGKGYNYLPIWKDRMD SRTLVPTPHADVYYSMNYLDLKETGPLVVAAPKVIGMFTDFFQRTITDVGLIGPDRA RGGLYLLLPRNYDGEVPKGYFTTSGTINNVFLFFRTVMKKGENGADFSDAVKLAEQTR IYPLMDEEKNIQPMKFPNASGQRINNMYFTDFSYWEKNKQFVDEEPISAISPELRGVLASIGIVKGKFPNTYSEKQLLEKAVKTAPKMITAQRLLGRKDERNLYYKDRQYERAWA
                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:AAA64344.1 (L16865)
52 in 129 aa"
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/transl_table=11
/transl_table=11
/product="putative peptide methionine sulfoxide reductase"
/protein id="BAC61644.1"
/db_xref="GI:28808467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement (1835. .2314)
/gene="VPA0301"

complement (1835. .2314)
/gene="VPA0301"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYKLHLPANPPAKLFWAVTLYNVVDGTMPETSQLLPSKNGFDNIEKNTDGSIDLYFGF
QLPNGAPESNYIKTIPGRDFLTAIRLYGTGIEFFDQTWKPDDVLKIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATSEYMQESYLDIDQRAAFFQYAYSSAPAMVMRTMNAGSKYPFTVRDSKGDILNGSH
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/- "----"-"
/- "----"
/- "----"
/- "----"
/- "----"
/- "----"
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|dentity 57 in 158 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .303450
                                                                                                          gene="VPA0303"
                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="VPA0302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to I
dentity 68 in 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="VPA0300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="VPA0300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="03:K6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Vibrio parahaemolyticus"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _strain="RIMD 2210633"
                                             to GB:AAL20622.1 (AE008775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to EMB:CAC46187.1 (AL591787) percent
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                                                                                                                                                                                                                                                                                                                                                                    percent identity
                                               percent
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gene

SgS

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complement (6548. .7201)
/gene="VPA0307"
/gene="VPA0307"
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/gene="VPA0307"
/gene="VPA0307"
/gene="VPA0307"
                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="VPA0306"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSAFAPSNLIPGIEPSEDRLLQGRLFAYADTQLYRLGANLFQLPVNRPLTSVNNHNQN
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RGnyfkmdlyvkvlspealskldyngldatkvmlnvfdrkvgtmytlnrlpenfflete
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4319. .5860
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/gene="VPA0304"
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complement (3733. .4089)
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Gylkryhgaafalogddidtrleyrfdikotlankaadlapnetylieggsanalla
RTLAERGDUTIITPSA YIAHLIRNTSANIILLGGYYOHOGESLVGFLTKLCIENIHFS
TAFLGIDGFHODTGFTSRDMMEADIABAILAKKRRNIVLTDSSKFGQIYPSSIGKTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="G1:28808470"
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QGLDGGFYSAEQVSQTSNGAALLVFYSSDIHATLEKVAKFGGQIIRPIFEFPGGCRFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                       /product="AnkB protein"
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/db_xref="GI:28808472"
                                                                                                                                                                                                                                                                                                                                                                 5992. .6429
/gene="VPA0306"
/note="similar to GB:AAF94738.1 (AE004235)
identity 63 in 152 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to REF:NP_231225.1 (NC_002505) percent
identity 83 in 510 aa"
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/evidence=not_ex
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rsmneqdrsdlianlagdlnkvidkdikatmvsyfyradkeygsrlaeatdtnlsqvk
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/db_xref="GI:28808471"
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identity 76 in 117 aa"
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                                                                         codon_start=1
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/transl_table=11
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'transl_table=11
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   TCAAACCTGTTTACGAGG 797
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YTSVLLFALDKEFLVADIISAYQEFGIDISRWTIKRRLIDSGVLKPTNKVASTUKGKG
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                                                                                                                                                                                                                                                                                                                                                                                                                        complement (7234. .7959)
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identity 60 in 241 aa"
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                                                                                                                                                                                                                                                                                     experimental
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Score 282.8; DB 1 Pred. No. 6.9e-72; DB 1; Length 303450;

TGCGCCGAAATCTATCCAGGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTG 179 TGCCGATAAAGGATTGGAAGTGTTGCTGATTAAACGTTCAAATCCGAATCGGCCTTACCA Mismatches 247; Indels 0 7856 0

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CDS gene

ACGTCCGGCGGATGAAAACTTTGAAGCGGCGCGCGACGCATTTGCCGGCGAGAAGATTCA AGAACCTGTCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCA TGGTGTCTGGGCATTACCGGGCGGGTTTGTCTTTGATAAAGACTTGACCAGCGAAGGCGG

299

7796

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419

7676 359 7736

7616

CAACAATGCTGGCGTGCCCGAGTGTCAGCTCAAATGGTTCCCATTGCAGGCGATCCTCAA AGAAGATTTTGGTATCGACCCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAA 479

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CDS

TĠĠŖĠŖŖŖŖĊĊĊŢŖĠĊŖŢŢŢĠŔĊĊŔĊĊŖŖŖŖŖĸĸĸĊŔŢĊĠŖŖŖŖŖŖĠĊŖŢĠĠĊŖĠŖŖŖŖĊŢ 7496 AGAAGAAATGCCGCTGGCTTTTGATCATGTCGCGCAAATTCAGCATGCGTGGCAAAAATT

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599

539

7556

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TTATTGATGCCTACGCCAAATTTGGCGTCGAAGTTAATCGCATGACCATTAAACGCCGCT
                                                   HBRAGAAHYWMBMMYBAKCHCMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNNNNATCARDD
                                                                                                                                                        AWYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHYGYKWNTRWWBWSHTWB
                                                                                                                                                                                                         TGCCGCTGGCTTTTGATCATGTCGCGCAAATTCAGCATGCGTGGCAAAAATTACGCGCTG
                                                                                                                                                                                                                                                             CYWKSMTNGKSHRBAAAVYTWYMWWRRYAHANNNWDYWWKACTWYKYBVCSKWWNNYA
                                                                                                                                                                                                                                                                                                           TTGGTATCGACCCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                               BGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWKMKTYWNN
                                                                                                                                                                                                                                                                                                                                                                                                           HBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNNGTTMWKRMWAWYWKMDMDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACGCGATCCGAATGGTTGGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTW---KSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNWTYKKAR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCATTGCCTGGCGGGATAGTGTATGACGAAGATATGACCGCTCATGGTGGAGAACCTG 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCTATCCAGGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGTAAAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTATTAGGGAAGCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTTGCGCCGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCKYRRWYNNKSRWWKGWYKKKWYBCANNTSBRYHARRWKDMKTAYBMTMTNKWGKTGWR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACAAAGTCTTATTTACATTTGACCATCATCATGCACTTACCTAAAATAAGCCCGTTGT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCATACTTATC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGRMRNYMVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNAKAMCKRAKYWGWNRABVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="consensus sequence of A.t., L.a.,
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                                                                                                                                        Direct Submission

All Submitted (10-JAN-2003) Whitchead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 14693)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Barran, N., Bastien, V., Bloom, T., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Karatas, C., Lui, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McChen, C., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., MacLean, C., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Feterson, K., Phuhkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Stange-Thomann, N., Stojanovio, N., Stubbs, M., Tayers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Melldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Comnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Nirson, S., Shalagan, C., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Mus musculus
SEQUENCE, 7 u
Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 23, 2003 this sequence version replaced gi:28275009. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 146963)
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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HTG; HTGS_F
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_PHASE1; HTGS_DRAFT
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unordered pieces.
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RP24-224A19 map
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WORKING DRAFT
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FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid, n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 145843 bases at least Q40 Consensus quality: 146107 bases at least Q30 Consensus quality: 146232 bases at least Q20 Insert size: 146000; agarose-fp Insert size: 146303; sum-of-contigs Quality coverage: 15.4 in Q20 bases; sum-of-contigs Quality coverage: 15.4 in Q20 bases; sum-of-contigs
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
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2264
5397
                                                                                                              /note="assembly_fragment
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
5497. .11945
                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:left"
                                                                                                                                                               140377.
                                                                                                                                                                                                             39505. .140276
                                                                                                                                                                                                                       /note="assembly_fragment"
19789. .39404
'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
12046. .19688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                     vector_side:right"
                                                                                                                                                            /note="assembly_fragment"
[40377. .146963
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/clone_lib="RPCI-24 Male Mouse BAC"
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    Summary Statistics

52.7%;
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Score 40.2; DB 2; Pred. No. 3.5;
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                      Length 146963;
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1819 AATGGAAGAATATTCAGTTTATACTTTAAAAAGCAAATCGTCTGACTTTATTTGAATTC 1878

452 ATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGATCATGTCG 511

Matches Query Match

91;

Conservative

0;

Mismatches

85 ;

<u>.</u>

Gaps

0

Local

Similarity

51.7%;

Score 40; I Pred. No. 2.

DB 3; 6

Length 2067; Indels

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123582 ATTGGTCAATTAAGAGAAGCAGAAGCTTTTCTTCTGTGTCCAGAGAAATTAAAAGTCGAA 123641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123522 CAGATGAAAGGAAGATTTTTTGGCGCTATCCACAAACTCTGCATTCACTTAAGAAACAATA 123581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 CAAACAAATAGAAGATTTTGGTATCGACCCCGAGCGCGCTAATTGGTTTGATCTTCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
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1 (Dases 1 to 2067)

Da Lage, U.-L., Van Wormhoudt, A. and Cariou, M.-L.

Diversity and evolution of the alpha-amylase genes in animals Biologia 57 (11), 181-189 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ceratitis capitata (Mediterranean fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-APR-1999) Populations, Genetique et Evolution, C.N.R.S., Avenue de la Terrasse, Gif sur Yvette cedex 91198,
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AF146758
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                                           AFTLAYPYGITRVMSSFDFVEHDQAPPADADEVILS PQFDTAGACMNGWVCEHRWRQI
YNMIGFKNAVRGTEMSNWWDNDDNQIAFCRGNRGFIAFNGNNWELTQRLYTCLSAGVY
CDVISGALVNGKCTGKAVLVDEWGFADIKLGADEFDGVLAIHVQAKMEERKERLERNL
                                                                                                             /LIBISIBLEON="MIAANRIGYCTAVILTILAAVSAQHEPHWLASRNTIVHLFEWKW
TDIAAECERFIAPRGFAGVQVSPVAENVVIDGRPWWERYQDYSKLITRSGNETEFAD
WYRRCNDVGYRIYUVULATAHGATHEGAVYGTGGSVAPARKYFPAVPYTEEDFHDTC
DIQDWIDRYQVQNCELICIKDLOGSSVRVETHLAFELNYLVELGVAGFRVDAAKHIPA
EELKIIYDNVVNLNTAHGFPFNARPFIYQEVVDHGYEAVSKYEYSPLGAVTEFRFSEE
IGGAFRGHQIKWLENWGPAMGFLPSAHAFYFVDNHINQREGGRVLTYKNAKQYKVAT
                    IRLLATRACROCHLYLILKLKCAPCIKIMEEYSVYTLKSKSSDFYLNSRRYFVMK"
                                                                                                                                                                                                                                                         product="putative amylase-related protein"
protein_id="AAO13692.1"
/db_xref="GI:27447663"
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\u00e9ene="Amyrel"
\u00e9ene="."
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/db_xref="taxon:7213"
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                                                                                                                                                                                                                                                                                                                                                                                   gene="Amyrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Ceratitis capitata"
|mol_type="genomic DNA"
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oin(71, .262,332, .805,878, .1903)
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Drosophila melanogaster (fruit Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10210833 by the submitte
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1 (bases 1 to 16237)
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AC012853
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                                                                                                                                                           CACATGCGAATGTATGAATATAAATTGTAGACGGCGAATATTGTGCATAATCAACGTAGA
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This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
Location Qualifiers
                                                                                                                         TTTGGCGTCGAAGT 641
                                                                                                                                                                                             ACTATTTTCATTA--GAAAAAGAGTTTTTAGTGGCGGATATTATTGATGCCTACGCCAAA
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ilarity 47.5%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 5.5;
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67158 GGTAAÁAATTÁTCATTÁÁÁCGCGÁATTGÁÁTGGGTGAATCTAAÁATÁTTACTGTTAÁCAT 67099
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                                                                                                                       149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.B., Galle, R., George, R.A., Harris, N. L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory, MS 64-121, Berkeley, CA 94720, USA
On May 12, 2001 this sequence version replaced gi:6958011.
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1 (bases 1 to 74085)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Celniker, S.E., Adams, M.D., Kronmiller, B.
                                                                                                                                                 Similarity
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Drosophila melanogaster
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AC012650
AC012650.8 GI:14028960
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                                                      egirearecaaccecaaaceceaaceceariceaaregirearecaerarireceariacec
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                                                                                                             4.9%;
ilarity 47.5%;
Conservative
                                                                                                                                                                                                                                                                        Drosophila melanogaster
pBeloBAC11)"
                                                                                                                                                                                                                                                                                  /map="19E-19E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Drosophila melanogaster"
|mol_type="genomic_DNA"
|strain="y; cn_bw_sp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Qualifiers
                                                                                                                 Score 39.2; DB 3;
Pred. No. 6.5;
0; Mismatches 163;
                                                                                                                                                                           Length 74085;
                                                                                                                       Indels
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                                                                                                                    Gaps
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390 TTTATTAAACCCGTGGAATGTCAAACAAATAGAAGATTTTGGTATCGACCCCGAGCGCGC 449

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TITLE
JOURNAL
REFERENCE
AUTHORS
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AC011761
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISM Drosophila melanogaster

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae; Drosophila.

Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Gonzalez, M., How, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb J., Paragas, V., Park, S., Patel, S., Pfelifer, B.,

Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Sequencing of Drosophila chromosome X, region 19E-19E

Lupublished

2 (bases 1 to 108350)
                                                                                                                                                                                                                                                                                                                                                                                                      Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clasioka, L., Doyle, C.M., Farfan, D.B., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Paccleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, B., Poon, L., Sequeira, A., Sethi, H., Snir, B., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                        Submitted (14-OCT-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Sep 6, 2001 this sequence version replaced gi:14280137. Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster, chromosome BACH50G05, complete sequence. AC011761.14 GI:15451480 HTG.
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                                                                                                                                                           Submission
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BE, BAC clone
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AUTHORS
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AE003571/c
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KEYWORDS
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Drosophila melanogaster (fruit fly)

Eukarycta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukarycta; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;

Rooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

C2 1 (bases 1 to 302540)

RS Adams,M.D., Celniker; S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D.,
Brandon,R.C., Rogers,Y.H., Blazej,R.G., Nelson,C.R., Gabor,G.L.,
Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,G.L.,
Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M.,
Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S.,
Borkova,D., Botchan,M.R., Bouck,J., Bexstein,P., Beasley,E.M.,
Bartis,K.C., Busam,D.A., Butler,H., Cadieu,E., Cencer,A.,
Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B.,
Davies,P., de Pablos,B., Delcher,A., Downes,M.D., Dew,I.,
Dietz,S.M., Dodson,K., Doup,L.E., Downes,M.D., Dugan-Rocha,S.,
Ferriera,S., Fleischmann,W., Fosler,C., Gabrielian,A.E., Garg,N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster chromosome complete sequence. AE003571 AE002620 AE014298
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/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBeloBAC11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila m
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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47.5%;
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CE 2 (bases 1 to 302540)

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., Celniker, S.E., Adams, M.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Busan, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Busan, C.A., Gocayne, J.D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, B., Galle, R.F., Garg, N.S., George, R.A., Gorzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pefeffer, B., Phouanenavong, S., Pittman, G.S., Patel, S., Feithards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tylar, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M. Sequencing of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., McLeod, M.P., McSherfi, A., Mount, S. M., Moy, M., Murphy, B., Murphy, L., Mount, S. M., Moy, M., Murphy, B., Murphy, L., Mount, S. M., Noy, M., Murphy, B., Murphy, L., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Sunces, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Siapleton, M., Strong, R., Sun, B., Svirskas, R., Tector, C., Turner, R., Weinstock, G. M., Waissenbach, J., Williams, S. M., Woodaget, Weinstock, G. M., Mang, Z.Y., Wang, Z.Y., Wassarman, D.A., Weinstock, G. M., D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zhong, W., Zhou, X., Zhu, X., Smith, H.O., Globs, R.A., Myers, E. W., Rubin, G. M. and Venter, J.C.

The genome sequence of Drosophila melanogaster
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Misra,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L.,
Misra,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L.,
Campbell,K., Hradecky,F., Huang,Y., Kaminker,J.S., Prochnik,S.E.,
Smith,C.D., Tupy,J.L., Bergman,C.M., Berman,B.P., Carlson,J.W.,
Smith,C.J., Tupy,J.L., Bergman,C.M., Bemert,D., Frise,E., de
Grey,A.D.N.J., Harris,N.L., Kronmiller,B., Marshall,B.,
Millburn,G.H., Richter,J., Russo,S., Searle,S.M.J., Smith,E.,
Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M.,
Rubin,G.M., Mungall,C.J. and Lewis,S.E.
Rubin,G.M., Mungall,C.J. and Lewis,S.E.
                                                                                        Direct Submission
Submitted (23-JAN-2003) University of California Berkeley, 539
Sciences Addition, Berkeley, CA 94720, USA
On Sep 13, 2002 this sequence version replaced gi:10726981.
                                                                                                                                                                                                                                                                                         Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA 6 (bases 1 to 302540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 302540)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                   FlyBage
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                             Location/Qualifiers
      /organism="Drosophila melanogaster'
                                                                                                                                                            gene
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                                                                                                                                                                                                                     /protein_id="AAF50917.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (56521. .57280)
/locus_tag="CG12679"
/note="last curated on Wed Jul 03
                                                                                                                                                                                              DSCNEGLSNVVETLGNTGILALMTYALTEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBgn0031103"
complement(56578. .57150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FLYBASE:FBgn0031103"
complement (56521. .57280)
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complement(join(47533. .47774,48345. .48708))
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/map="1924-1924"
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DQQSEEKSESKEERIFQMELFE"
transposon="H-element{}182"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CG12679 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (47533. .47774, 48345. /locus_tag="CG15462"
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                                                                                                                                                                                                                                                                                                                                                                                                                'product="CG12679-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locus_tag="CG12679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            map="19C4-19C5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="CG15462-RA"
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|011n(8252. 8476,8536. 9439)
|1ocus_tag="CG1631"
|product="CG1631.RA"
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/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="FLYBASE:FBgn0031102"
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                                                                               ACI35793.3 GI:38153795
HTG; HTGS PHASE2; HTGS ACTIVEFIN.
OTYZE SETIVE (japonica cultiver-group)
OTYZE SETIVE (japonica cultiver-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzea; Oryzea.
1 (bases 1 to 12868)
1 (bases 1 to 12868)
Event Common Commo
                                                                                                                                                                                                                                                                                                                            128683 bp DNA linear FORYZA SATIVA (japonica cultivar-group) chromosome 11 OSJNBb0017P15, *** SEQUENCING IN PROGRESS ***.
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,
Overton II,L., Tsitrin,T., Kim,M., Bera,J., Jin,S., Fadrosh,D.W.,
Tallon,L., Xoo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATCAAAACAGGCATAAAAACTGAATACCAGCCAATACTACCGTAAACAGATTCCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTACTAACTTGTTTAATTGCAAGTAAACTGGAAATTTAAGTGTATTCAAATAATTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGGACTCGGACT 302029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGCAAATTCAGCATGCGTGGCAAAAATTACGCGCTGCGGTTGAATACACATCCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANATAGIATATATCÍTTTTAAAACGCCÁCGAAAGAAAAGCCTATATCAGTTCTAAATGT
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/map="19C5-19C5"
62674. .63120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:7295606"
/db_xref="FLYBASE:FBGN031104"
/translat.on="MSGNFXMENPNNESHSYFLRNIFEELOPOFTRGFNQWMGNOST
MTKGLPSNTVNKSAQTASVNDGNLQASVIAMLAGMDSILDMEQPNRSPSRESHERLNE
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/locus_tag="CG15460"
/note="CG15460 gene product"
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/note="last curated on Wed Jul
/map="1905-1905"
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/db_xref="FLYBASE:FRA
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complement(71194. .71526)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%;
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lement(71194..71526)
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0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.2;
Pred. No. 7.
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AUTHORS
         RESULT 13
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Best Local Similarity
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                                                                                                                              50504
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On Nov 4, 2003 this sequence version replaced gi:24431631.

* NOTE: This is a 'working draft' sequence. It currently
consists of I contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 128683: contig of 128683 bp in length.
1 128693: contig of 128683 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 GCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 TTACGCTTTATTAAACCCCGTGGAATGTCAAACAAATAGAAGATTTTGGTATCGACCCCGA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
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Medical Center Dr, Rocky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell,R.
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                                                                                                                                                                                                                                                                                                                                                                     WMAAWMYRCMTKRGTGASWWKMSASAAAKYMAWYCRMRKRRKWKASYTRMKWKRNARWMA
                                                                                                                              HWWSAWSRRYWWSMSWMRMKRSYRWKYYAKWCAYYRMWWASYY 50462
                                                                                                                                                                                    CGTTTATCGTCTTGCCAGTCATGAAGTCACCTATTTTCAAACC 786
                                                                                                                                                                                                                                                                                                         GATCGTCAGTACCAATAAAATGGCCGCATCTTGTAAAGGCAAAGGAGCCAAACCAGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                       CAPATTTGGCGTCGAAGTTAATCGCATGACCATTAAACGCCGCTTGATCAATACCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMYRSAWYSWTSYMKAMYRRGSWCMAYWYRKMMAAMYWTGYMKWRKWGRGAMWMYWCRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTGGTACTATTTCATTAGAAAAAGAGTTTTTAGTGGCGGATATTATTGATGCCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWYKKSTTTGCAMMWTAKGKKMYGKWSKTWTGSCYKKRYWRAWYCYKWSMKRKMKSYAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATGTCGCGCAAATTCAGCATGCGTGGCAAAAATTACGCGCTGCGGTTGAATACACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WMMACMWWWKMMWWYCYWKAYMWRATWTTAWSACTTGCGAWYTCYTTGGRKMYRKTCT
                                                                                                                                                                                                                                                TWYRHGRARWMYMRMKMBWYTKMMARRAKRWAYRARAASSSMAKRRRTYRMSASSRKKMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
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chromosome="11"
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Pred. No. 7.9;
70; Mismatches 185;
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50625

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REFERENCE AUTHORS TITLE

KEYWORDS ACCESSION DEFINITION

ORGANISM

REFERENCE

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AL Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 168422)

RS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastlen,V., Bloom,T.,
Boyuslavkiy,L., Boukhgalter,B., Corum,B., DeArellano,K.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Newlygen,C., Nicol,R., Norbu,C., O'Comnor,T., O'Donnell,P.,
O'Meil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stoubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                        Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2003 this sequence version replaced gi:28201661. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (Dases 1 to 100424)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Birren,B., Earna,N., Bastlen,V., Bloom,T., Boguslavkly,L.,
Anderson,S., Barna,N., Bastlen,V., Campopiano,A., Chang,J.,
Ponthralter.B. Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
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Mus musculus clone RP24-252P2, WORKING DRAFT SEQUENCE, 6 unordered
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Birren,B., Nusbaum,C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
   Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                  138073 ATATTGCTGAAAAACAGTCCTTATCAAGAATTGTGTTCAGGGATTACAATCAACAACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                            568 GTACTATTTCATTAGAAAAAGGTTTTTAGTGGCGGATATTATTGATGCCTACGCCAAA 627
                                                                                                                                                                                   508 GTCGCGCAAATTCAGCATGCGTGGCAAAAATTACGCGCTGCGGTTGAATACACATCCGTG
                                                                                                                                                                                                                                                                                                                                 448 GCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 163000; agarose-fp
Insert size: 167922; sum-of-contigs
Quality coverage: 12.7 in Q20 bases; agarose-fp
Quality coverage: 12.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; n/a; 100% of read Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Chemistry: Dye-terminator Big Dye; 100% of re Chemistry: Dye-terminator Big Dye; 100% of re Chemistry: Dye-terminator Big Dye; 100% of read Consensus quality: 167327 bases at least Q40 Consensus quality: 167845 bases at least Q20 Consensus quality: 167845 bases at least Q20
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Center clone name: 252_P_2
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/db_xref="taxon:10090"
/clone="RP24-252P2"
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clone end:T7
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115287. .151317
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11741: gap of 100 bp
14593: contig of 2852 bp in length
14693: gap of 100 bp
78832: contig of 64139 bp in length
78932: gap of 100 bp
115186: contig of 36254 bp in length
115286: gap of 100 bp
151317: contig of 3631 bp in length
151417: gap of 100 bp
168422: contig of 17005 bp in length
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RS Birren, B., Linton, L., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Chown, A., Canarata, J., Campopiano, A., Chang, J., Chazaro, B., Chown, A., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dear, K., Diaz, J.S., Dodge, S., Farc, S., Gord, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Gride, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norman, C., Wicol, R., Northu, C., Norman, C., H., O'Connorl, P., O'Neil, D., O'Nei
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ALTECT Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome AL Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE3 (bases 1 to 187063)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Birne, B., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslawkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., DaArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galgyan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., 1liev, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Vones, C., Macdonald, P., Major, J., Manning, J., Mathhews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Mathhews, C., McCarthy, M., Mendurin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Nguyen, C., Nicol, R., Peterson, X., Phunkhang, P., Ferre, N., O'Neil, D., Glauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tavers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., V
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AC107808.11 GI:39841185
HTG; HTGS PHASE2; HTGS FULLTOP; HTGS ACTIVEFIN.
Mus musculus (house mouse)
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RP23-61B14
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ne 9 clone RP23-61B14 map 9,
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Best Local
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                     Homo sapiens cDNA FLJ43506 fis,
AK125495
AK125495.1 GI:34531609
                                                                                                                                                    AK125495
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Submitted (18-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 13, 2003 this sequence version replaced gi:38490669.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 4.9%;
Similarity 46.2%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the finished sequence as soon as it is available the accession number will be preserved.

1 34741: contig of 34741 bp in length 34742 34841: gap of 100 bp 34842 104257: contig of 69416 bp in length 104258 104357: gap of 100 bp 104358 187063: contig of 82706 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that he
                                                                                                                                                                          AGGAGATTAAAGATGATTGACACATCTTTGGCAGAAAAA 57591
                                                                                                                                                                                                             GTCAGTACCAATAAAATGGCCGCATCTTGTAAAGGCAAA .726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGCGCAAATTCAGCATGCGTGGCAAAAATTACGCGCTGCGGTTGAATACACATCCGTG
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                                                                                                                                                                                                                                                                                                                                           TTTGGCGTCGAAGTTAATCGCATGACCATTAAACGCCGCTTGATCAATACCGGGGTGATC
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Center clone name: 61_B_14
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RPCI-23 Female Mouse BAC"
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Pred. No. 8.2;
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mRNA linear
clone PERIC1000147.
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SOURCE
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Search completed: April 30, 2004, 15:29:03 Job time : 3230.8 secs
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TITLE
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Local Similarity 53.2%;
hes 82; Conservative (
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I Isogal, T. and Yamamoto, J.

Isogal, T. and Yamamoto, J.

Direct Submission

Submitted (15-UUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                             GGTTGGAGTGTCAGTATTTCCCATTACGCTTTAT 394
                                                                                                                TTTTTCAGAGACTTTCATTTCTGTTACATTGGAT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="pERIC1000147"
/tissue_type="pericardium"
/clone lib="pERIC1"
/note="cloning vector: pME18SFL3"
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Listing first 45 summaries
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Maximum DB
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Score
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1: geneseqn1930s:*
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3: geneseqn2000s:*
4: geneseqn2010las:*
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Ada71938 Rice gene
Ada71938 Rice gene
Aba18862 Human ner
Aba18863 Human ner
Aba18866 Human ner
Aba18866 Human ost
Adc90659 E. faeciu
Adb76952 Mouse CLC
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ABA90521 ADA70920 AAS37288 ACA28161

Ada70920 Rice gene Aas37288 Novel hum Aca28161 Prokaryot

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

P-PSDB; ABU49658.

2003-029926/02.

(ELIT-) ELITRA PHARM INC.

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Zamudio C, Trawick JD,

Malone C, Carr GJ,

Haselbeck R, Yamamoto R,

Ohlsen Forsyth

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Zyskind Xu HH;

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Claim 14; SEQ ID NO 41398; 1766pp; English.

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Aas93830 DNA encod	Aca54254 Prokaryot	Aaq03541 Chinese h	Aca32678 Prokaryot	Aas52644 E. coli D		Aaf86431 Pyrococcu		38		Pa	-	Aah24065 Yeast AOD	Aac35493 Arabidops		510	Abq26306 Oligonucl	Continuation (18 o	Continuation (19 o		Aad47845 Haemophil	Aai85726 Human pol

ALIGNMENTS

RESULT 1 ACA53528 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-0094893. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107. 03-OCT-2002. WO200277183-A2 Vibrio cholerae. Antisense; ds; prokaryotic essential gene; Prokaryotic essential gene 19-JUN-2003 ACA53528; ACA53528 standard; DNA; 717 design; gene. (first entry) #35185. BP cell proliferation,

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cc nucleic acid; (2) a host cell containing the vector; (3) an isolated cc polypeptide or its fragment whose expression is inhibited by the cartisense nucleic acid; (4) an antibody capable of specifically binding cc the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for cc proliferation or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) cl identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent cc which each of the strains is present in a culture or collection of constitying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational constitution of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational constitutions of an expension of a screening homologous nucleic acids required constitution of an expension of a screening for homologous nucleic acids required constitution of an expension of a screening homologous nucleic acids the target constitution of a part of the printed specification, but was obtained in celectronic format directly from WIPO at the carget for homologous included in the printed specification, but was obtained in
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                                                                                              GIGGTACTATTTCATTAGAAAAAGAGTITTTAGIGGCGGATATTATTGATGCCTACGCC
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   AAATTTGGCGTCGAAGTTAATCGCATGACCATTAAACGCCGCTTGATCAATACCGGGGTG
                                                               GTAGTGCTGTTCTCACTTGAGCTGGAGTTTTTGGTGGCGGACATTATTGAGGCTTACGCC
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The present invention relates to novel cell growth, differentiation and death (CGDD) proteins and polymocleotides encoding them. The sequences of the invention are useful in diagnosing, preventing and treating disorders associated with an abnormal expression or activity of CGDD such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cell growth, differentiation and death protein; CGDD; leukaemia; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; muscular disorder; myotonic dystrophy, catatonia, endocrine disorder; diabetes; Grave's disease; cancer; immunological disorder; scleroderma; systemic lupus erythematosus, allergy; Crohn's disease; renal disorder; gastrointestinal disorder; globasture's syndrome; infection; cirrhosis; cardiovascular disorder; atherosclerosis; hepatic disease; transgenic; transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic; dermacological; immunosuppressive, carebroprotective; anticonvulsant; antiparasitic; fungicide; virucide; uropathic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001US-0340747P.
20-DEC-2001; 2001US-0342761P.
15-JAN-2002; 2002US-0349705P.
06-FEB-2002; 2002US-0354764P.
12-FEB-2002; 2002US-0356216P.
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                                                                                                                                                                                                   New CGDD polypeptides, useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of CGDD, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.
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Burrill
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Swarnakar A, Lee S,
WW, Lee SY, Khare R,
JD, Blake JJ, Ho A, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCYTE GENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramkumar J,
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Gorvad AE,
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غE, Yue H, Lee EA, Beci
Ison CH, Hafalia AJA, T
ماماله AR, Gietzen KJ,
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                     comprises identifying a gene
the incompatible interaction
                                                                                                                                                                                                  Identifying at least one gene involved in plant resistance or pathogenic infection for conferring resistance or tolerance to bacterial, fungal or viral infection by determining or detection
                                                                                                                                                                                                                                                                                                                                           Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease), muscular disorders (e.g. myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis) and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to create humanised animals or transgenic animals to model human diseases. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
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                                                                 The present invention relates to a method (M1) for identifying involved in plant resistance or response to pathogenic infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-IB001105
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                              ACCAGCCACCGTTTATCGTCTTGCCAGTCATGAAGTCACCTATTTTCA 782
                                                                  KYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCK
                                                                                               TACCGGGGTGATCGTCAGTACCAATAAAATGGCCGCATCTTGTAAAGGCAAAGGAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRWSAWRYCSRMKCAKTKYASSARWTKRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGTAAATGGGCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTTGCGCCCGAAAT-CTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWMWWRYTMYTYCYAMTCAKCKYKWAMTKWWTTWACAWRATSWRWRAMAGMRWKRYKMKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTTACATTTGACCATCATCATGCACTTACCTAAAATAAGCCCCGTTGTTTATTAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCGATCCGCTGGTTGATGGCAACCC---CAAACGCGATCCGAATGGTTGGAGTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCATACTTATCCTAATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 335; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB
Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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88
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                                                                                                                                   196
                                                                                                                                                                    674
                                                                                                                                                                                                                                       614
                                                                                                                                                                                                                                                                                                         554
                                                                                                                                                                                                                                                                                                                                          376
                                                                                                                                                                                                                                                                                                                                                                           494
                                                                                                                                                                                                                                                                                                                                                                                                           436
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 5263; 899pp; English.
                                             1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene,
                                                                                                                                                                                                                     398
                                                                    578
                                                                                                                    518
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                                                                                                                                                                                             876
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                                                                                            996
                                                                                                                                             936
                                                                                                                                                                                                                                            816
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                                                                                                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                GCAACCCCAAACGCGATCCGAATGGTTGGAGTGTCAGTATTTCCCATTACGCTTTATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                             CATT
                                                                                                                                                                                                                                           TYWTGTWAAWWMAKTKMRMGMTGAKTRGRARKARYWWKWATWCATKRWMTKGKGAKWAWT
                                                                                                                                                                                                                                                                                                                   GTATTTGTCGGCAAAAAGTCCATACTTATCCTAATTTTATCAGCGATCCGCTGGTTGATG
                                                                     CATT 581
                                                                                                                                                                                                                                                                                             MA-RMMWKTRAWSKSYARAYWKMAGCACCTACACACACAGAAATGTTGTTTTATTTC
                                                                                                                    TTCAGCATGCGTGGCAAAATTACGCGCTGCGGTTGAATACACATCCGTGGTACTATTTT
                                                                                                                                             RWGWTKYWYWYCTTWKWACGRATKYMCCAGWWAMYSYSWTRTYWMRTWRWMWASSRTAKR
                                                                                                                                                                TTGATCTTCATACTTTACTCAAAGAAGAATGCCGCTGGCTTTTGATCATGTCGCGCAAA
                                                                                                                                                                                             WAKAWRKYYWSWWRAWYYYYKTRTRYKTCWWKARWGSWAYWRMWWKGSAKWWWMWKGG
                                                                                                                                                                                                                   ACCCGTGGAATGTCAAACAAATAGAAGATTTTGGTATCGACCCCGAGCGCGCTAATTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                             Conservative 128;
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                                             1058
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                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; fungal infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5263
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                                                                                                                                                                                                                                                                                                                                                         4.7%;
15.8%;
                                                                                                                                                                                                                                                                                                                                                         Score 37.6; DB 7;
Pred. No. 0.56;
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Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                             127;
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                                                                                                                                                                                                                                                                     397
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RESULT 5 ABA18862

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Human nervous
                                                                           ABA18862 standard; DNA; 438 BP
                        (first entry)
system related
polynucleotide
SEQ ID
ö
11193.
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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; Human; nootropic; neuroprotective; cytostatic; immunosuppressive; antiinflammatory; anti-HIV; dermatological; , virucide; vulnerary;

ds.

07-JUL-2000 11-JUL-2000 11-JUL-2000 14-JUL-2000 26-JUL-2000 14-AUG-2000 16-SEP-2000 17-SEP-2000 18-SEP-2000 18-SEP-2000 19-SEP-2000 31-JAN-2000; 19-MAY-2000; 16-AUG-2001 WO200159063-A2 neurological disease; infection; nephrotropic; gene therapy; vaccine; 2000US-0214886 2000US-0216479 2000US-0216680 2000US-02174869 2000US-02174969 2000US-02295499 2000US-02245199 2000US-02252149 2000US-02252149 2000US-02252149 2000US-02252669 2000US-02252679 2000US-02257599 2000US-02257599 2000US-02257599 2000US-022592497 2000US-022592497 2000US-022592497 2000US-022592497 2000US-02292497 2000US-02293439 2000US-02312439 2000US-0179065P 2001WO-US001334

2000US-0232080P. 2000US-0232081P. 2000US-0231968P. 2000US-0232397P. 2000US-0232398P. 2000US-0232398P. 2000US-0232398P. 2000US-0232398P. 2000US-0232399P.

2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0234998P. 2000US-0235484P.

2000US-0233063P. 2000US-0233064P. 2000US-0233065P.

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RESULT 6
ABA18863
ID ABA1
XX ABA1
AC ABA1
XX DT 23-J
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic canaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias, (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic confections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                          Matches
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                            Human
                                                                                          23-JAN-2002
                                                                                                                                                     ABA18863 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 438 BP; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 11193; 1701pp + Sequence Listing; English
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                                                                                                                                                                                                                                  264
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                                                            nervous
                                                                                                                                                                                                                                                                                                                                                         l Similarity
62; Conserv
                                                                                                                                                                                                                                                    AATAGAAGATTTTGGTATCGACCCCGAGCGCGCTAATTGGTTTG
                                                                                                                                                                                                                                                                                                                   GAATGGTTGGAGTGTCAGTATTTCCCCATTACGCTTTATTAAACCCCGTGGAATGTCAAACA
                                                                                                                                                                                                                                  AACCTAACATTTTGGTAGTCTCTGGGTTTGCTCTTTTAACTTTG
                                                                                                                                                                                                                                                                                              GGAAAGATAGAGTGCTGAGTATTCACATTACGCTTTATTTCAACTTGGAAATGATAAACA
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                                                                                                                                                                                                                                                                                                                                                         4.6%;
llarity 59.6%;
Conservative
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2000US-0251980P.
2000US-025198P.
2000US-0251850P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
2000US-0259678P.
                                                                                          (first entry)
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                                                            system related
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Pred. No. 0.48
0; Mismatches
                                                           polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                     Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                       0 Other;
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                                                                                                                                                                                                                                                              460
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2000US-0236367P 2000US-0236367P 2000US-0236369P 2000US-0236370P 2000US-0237037P 2000US-0237038P 2000US-0237039P 2000US-02370399 2000US-0237039935P 2000US-0240960P 2000US-0241785P 2000US-0241785P 2000US-0241808P 2000US-0241808P 2000US-0241808P 2000US-0246474P 2000US-0246477P 2000US-0246477P 2000US-0246477P 2000US-0246477P 2000US-0246477P

20-OCT-2000 01-NOV-2000 08-NOV-2000 08-NOV-2000

2000US-0246523P 2000US-0246525P 2000US-0246525P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-024651P 2000US-024661P 2000US-024661P 2000US-024920P 2000US-024920P 2000US-024921P 2000US-024921P

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
antirheumatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; delibera
Go antidibetic attilicary antiony laminatory; Co antidibetic attilicary anticovalisatic antilingal; Ci cardiant; Immune discreter order antifungal; Ci cardiant; Immune discreter order order antifungal; Ci cardiant; Immune discreter order or
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21-SEP-2000; 25-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-OCT-2000; 20-OC
2000US-023423P 2000US-023499RP 2000US-023499RP 2000US-023499RP 2000US-0235834P 2000US-0235834P 2000US-023637P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-023636P 2000US-02363703P 2000US-02363703P 2000US-023697 2000US-023703P 2000US-023703P 2000US-0241785P 2000US-0241785P 2000US-0241785P 2000US-024677P 2000US-024677P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-024677P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-024921P 2000US-0251160P 2000US-0251160P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-0251166P 2000US-025116P 2000US-02510B 2000US-02510B 2000US-025

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RESULT 7
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Best Local S
Matches 62
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                                                                                                                                                                                    antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                              Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiparkinsenia; hepatotropic; cerebroprotective; antiinflammatory;
                         16-AUG-2001
                                                                      WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                       Human nervous system related polynucleotide SEQ ID NO 11197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 438 BP; 130 A; 78 C; 104 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA18866 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 11194; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
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ilarity 59.6%;
Conservative
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encoding 3224 human nervous system antigen polypeptides,
                                      GENOME
                         sc,
                                      SCI INC
                         Ruben
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Nucleic acids

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RESULT 8
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AC ABQ881
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Best Local
Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
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                                                                WPI; 2002-557663/59.
                                                                                                               Ji D,
                                                                                                                                                                                            18-DEC-2000; 2000US-0255882P.
24-APR-2001; 2001US-0285691P.
                                                                                                                                                                                                                                                                                                          WO200250301-A2.
                                                                                                                                                                                                                                                                                                                                                                       osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human osteoblast differentiation related cDNA SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ88161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                              (GENE-)
                                                                                                                                                                                                                                           18-DEC-2001; 2001WO-US048276
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
                                                                                                                                                                                                                                                                                                                                                                                      osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                               Axelrod DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 59.6 62; Conservative
                                                                                                                                              GENE LOGIC INC.
PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAAGATAGAGTGCTGAGTATTCACATTACGCTTTATTTCAACTTGGAAATGATAAACA
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                                                                                                                                                                                                                                                                                                                                                                         osteopathic;
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                                                                                                               Cook JS,
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Pred. No. 0.48;
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Best Local S
Matches 84
New isolated nucleic acid derived from Enterococcus faecium encoding 
Enterococcus faecium polypeptide useful for detection, prevention and
                                             WPI; 2003-799836/75
P-PSDB; ADC94313.
                                                                                                                                                            02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC90659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis or male osteoporosis, osteopenia, osteodystrophy, druginduced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocycosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                               Doucette-Stamm
                                                                                                                                                                                                            30-JUN-1998;
                                                                                                                                                                                                                                            24-JUN-2003.
                                                                                                                                                                                                                                                                                                        Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                       ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC90659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition; (b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                                      E. faecium DNA sequence SEQ ID 286
                                                                                                                               (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 68; 78pp + Sequence Listing; English.
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                                                                                                                            GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTACATTTGACCATCATCATGCACTTACCTAAAATAAGCCCGTTGTTTATTAGGGAAG 79
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98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 10
ADB76952
ID ADB76952
AC ADB76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
   21-JAN-2002; 2002JP-00012180.
21-FEB-2002; 2002JP-00044981.
07-MAR-2002; 2002JP-00061668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Мив вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory; gastrointestinal; nephrotropic; respiratory disease; nephritis; digestive disease; mouse; CLCA4; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse CLCA4 gene SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003
                                                                                                                                                                                                                                                             WO2003062426-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB76952 standard; DNA; 1119 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 552 BP; 174 A; 96 C; 135 G; 147 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one if the disclosed E. faecium nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATATTGGGGATATCGATTTTTCAGACTTCGCTCTTATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATGGTTGGAGTGTCAGTATTTCCCCATTACGCTTTATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATACTTATCCTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCCAAACGCGATCC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGTCAAACAATCTCAGAAGATATCTATGTTTCGGGTGGCAGTCGGATTTTTCAAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGAACCTGTCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGT
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                                                                                                                                  2003WO-JP000408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           /product= "CLCA4"
/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.6; Di
Pred. No. 1.3;
0; Mismatches
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413

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RESULT 11
AAQ49902/c
ID AAQ499
XX AAQ499
XX AAQ499
XX DT 14-MAY
DT 04-MAY
XX Glutam
XX JP0523
XX JP0523
XX JP0523
XX GNITU
XX WPI; 1
DR P-PSDB
XX WPI; 1
DR P-PSDB
XX WPI; 1
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel protein comprising a sequence selected from two protein sequences each 924 amino acids in length. A protein of the invention has respiratory, gastrointestinal, and nephrotropic activity. The protein is useful for treatment, diagnosis and prevention of respiratory disease, nephritis, and digestive diseases. The present sequence encodes mouse CLCA4.
                                                                                                                                                                                                                                                                                                                                                                              14-MAY-2003
04-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ49902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ49902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 104; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakanishi A,
               WPI; 1993-331429/42.
P-PSDB; AAR42054.
                                                                                                                   26-FEB-1992;
                                                                                                                                               17-SEP-1993
                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                        Glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins
                                                                                       26-FEB-1992;
                                                                                                                                                                          JP05239098-A
                                                                                                                                                                                                                                                                                                          cell necrosis;
                                                                                                                                                                                                                                                                                                                                                    Glutamic acid
                                                          (MITU ) MITSUBISHI KASEI CORP
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DB; ADB76951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treatment, diagnosis and prevention of respiratory disease, s, digestive diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCACCTGGAGCCAACAAGCCCCTGCCATTCATCTCAGGGATCCCAAAGGAAC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCAAAGGAGCCAAACCAGCCACCGTTTATCGTCTTGCCAGTCATGAAGTCAC 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGATATTATTGATGCCTACGCCAAATTTGGCGTCGAAGTTAATCGCATGACCATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first en
                                                                                                                                                                                                                                                                                                          receptor; nerve; ; ischemia; ss.
                                                                                                                                                                                                                                                                                                                                                  receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morita
                                                                                       92JP-00039563.
                                                                                                                   92JP-00039563
                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                      product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
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                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        4368
                                                                                                                                                                                                      "glutamic_acid_receptor"
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•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                       synapse; synapse plasticity; cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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RESULT 12
AB199832/c
ID AB1998
XX AB1998
XX AB1998
XX AB1998
XX MOUSE;
XW WOSCOP
XX MOUSE;
XW VASCOP
XX MO2001
XX WO2001
XX HS-MAY
XX 18-MAY
XX 18-MAY
XX WPI; 2
DR P-PSDB
XX Examin
PT express
PT determ
PT genes:
YS Claim
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence was transformed into E. coli several clones coding the new glutamic acid receptor were obtained. The sequence is useful for the elucidation of nerve information transfer by synapses, expression of synapse plasticity and nerve cell necrosis caused by cerebral ischemia and also for the development of new drugs. In the specification the length of the sequence as given as 4392 bp The actual number of bases is 4368. The sequence may have a line missing or has been numbered incorrectly. (Updated on 14-MAY-2003 to correct PS field.)
                                          Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                              WPI; 2002-034733/04.
P-PSDB; ABB57341.
                                                                                                                                                                                                                                                                                                                                                                                   Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4368 BP; 1151 A; 1127 C; 1090 G; 1000 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein for elucidation of nerve information transfer by synapse comprises glutamic acid receptor of specified aminoacid sequence.
                                                                                                                                                             Ishikawa
                                                                                                                                                                                                                          18-MAY-2000; 2000JP-00145977
                                                                                                                                                                                                                                                         18-MAY-2001; 2001WO-JP004192
                                                                                                                                                                                                                                                                                         22-NOV-2001.
                                                                                                                                                                                                                                                                                                                        WO200188188-A2
                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABI99832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABI99832 standard;
                                                                                                                                                                                            (-INYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493
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                                                                                                                                                                                          VIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCGAATGGTTGGAGTGTCAGTATTTCCCCATTACCGTTTATTAAACCCGTGGAATGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGGAGAACCTGTCGATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 11; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATGGGGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAAATAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAACGTGGATGTCGGATCCTTGTCAGCCATGATCATAGATGCACCCCCATGAATGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTCCATACTTATCCTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATGAAGTCTCTGTAGCCAGGGAAGATGGTGGTGACCAAGGAGAAGACATGCCAGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%;
llarity 49.0%;
Conservative
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Pred. No. 4.
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<u>ب</u>

Page 2406-2415; 2690pp; English

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RESULT 13
ABO67196 4/c
ABO67196 4/c
Continuation (5 of 7) of
WP Sequence split into 7
WP ABO67196 0
WP ABO67196 1
WP ABO67196 3
WP ABO67196 3
WP ABO67196 4
WP ABO67196 5
WP ABO67196 6
                          RESULT 14
ABQ67196 5/c
ABQ67196 5/c
Continuation (6 of the continuation of the continu
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P Sequence split into 7
P Fragment Name
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ABQ67196_2
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Best Local S
Matches 55
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Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression is conclusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABI99702 to ABI99912, encoding the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4512 BP; 1197 A; 1156 C; 1122 G; 1037 T; 0 U; 0 Other;
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ABQ67196 2
ABQ67196 3
ABQ67196 3
ABQ67196 4
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RESULT 15
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CCGTTCCAGCTTTCATTAAAACAATCTTTT
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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10519.601 Million cell updates/sec
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Asmundson Hall, UCD, Davis, CA 95616, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2435_2, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 1-(530)-752-96
Email: akozik@atgc.
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA sprimed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSFORT 6 vector. Library was normalized."
/clone_lib="QH_M sunflower H.argophyllus"
/note="Vector: pBRcDNAsfiAB; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector.
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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/clone="QHM18L03"
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, (
85721-0088, USA
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         /sub_species="mays"
/db xref="taxon:4578"
/db xref="taxon:4578"
/clone="zwnyBB00194117"
/lab_host="DH10B"
/clone lib="zwnyBBb"
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/hote="vector: pBsloBAC11; Site_1: HindIII; Site_2:
/hindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .746
                                                                                                                                                                                                                                mol_type="genomic
cultivar="B73"
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47.8%;
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Pred. No. 0.53;
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Bharti, A.K., Messing, J

ΑZ

GSS 29-JUL-2003

JOURNAL COMMENT

FEATURES

source

REFERENCE AUTHORS

ACCESSION VERSION

KEYWORDS

ORGANISM

RESULT 2 CF088325

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                                                                                                                  287 CATÁCTTGATCAGCTACTGCAÁATTTÁGACAÁCTAACCAATGCAGTTGCCAATTAA 342
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1 (bases 1 to 826)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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PUBNS09TD ZM_0.6_1.0_KB
genomic survey sequence.
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Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                             GCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGA 503
                                                                                                                                                                          GCCTTATTAACTCCTAGGTTTCTCAAGCAGATAGATGAATCTGAAATCTGGCCAAAGTTC
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301-838-0208
1: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                      /clone="xxmgFa097A17"
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/clone_lib="ZM_0.6_1.0 KB"
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CoT selected genomic DNA libraTy"
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/mol_type="genomic n
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; eudicotyledons; Asteroideae;
Heliantheae, Helianthus.

1 (bases 1 to 438)

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QHM3F15.yg.abl QH M sunflower
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742
                                                                                                                             http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Helianthus argophyllus
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Unpublished (2003)
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1 (bases 1 to 919)

Whitelaw,C.A., Quackenbush,J., Var
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/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/strain="B73"
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Y., San Miguel,P., Ma,J. and
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Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OH_CA_Contig2435, see http://cgpdb.uc
                                                                                                                                                   Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THIS CHM12N04.yg.abl QH M sunflower H.argophyllus Helianthus argophyllus clone QHM12N0^4, mRNA sequence. CF087071
Department of Vegetable Crops, R.W.Michel University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742
                                                                                                        http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                            1 (bases 1 to 464)
Kozik, A., Michelmore, R.W.,
                                                                                                                                                                                                                                                                                    Helianthus argophyllus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Helianthus.
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EST.
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                                                                                   Contact: Alexander Kozik [R.W.Michelmore
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ilarity 47.3%;
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/note="Vector: pBRcDNASfiAB; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector. Details of library construction can be obtained at
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/mol_type="mRNA"
/db_xref="taxon:73275"
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                                                                  R.W.Michelmore
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           Unpublished (2000)
Contact: Robert B. Woundersity of Utah Goundersity of Utah Rm. 308, Biomedical 1
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                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I to 638)

1 (bases 1 to 638)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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1M0160C17R Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0160C17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                            Mouse whole genome scaffolding with
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/note="Vector: pBRcDNASfiAB; The library was construct/
from three different sources (seedling, root and leaf)
RNA from a single genotype. cDNAs were pooled and
directionally cloned into a custom medium-copy vector.
Details of library construction can be obtained at
http://cgpdb.ucdavis.edu/"
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'db_xref="taxon:73275"
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47.3%;
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                                                                                                                                                                                                                                                                                 sequence.
AJ539921
AJ539921.1
EST.
                Helianthus annuus (common sunflower)
Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 401)
1 (bases 1 to 401)
1 Tamborindeguy, C., Liboz, T., Petitprez, M. and Gentzbittel, L.
An expressed-sequence-tag database of the sunflower protoplast
Unpublished (2003)
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 638.
                                                                                                                                                                                                                                                                                                                                                                                       AJ539921 HaSemS3 Helianthus annuus cDNA clone HM0007,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/, resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Length: 10000 Std Erro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 1;
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EST.

EST.

Helianthus argophyllus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroideae;

asterids; campanulids; Asterales; Asteroideae;

Heliantheae; Helianthus.

E 1 (bases 1 to 435)

E 1 (bases 1 to 435)

E Nozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,

Lin, E., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
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QHM3P22.yg.abl QH M s
~nwa clone QHM3P22, π
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Institut National Polytechnique de Toulouse - Ecole Nation
Superieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde
Auzeville, CASTANET TOLOSAN 31326, France.
Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2415, see http://cgpdb.ucdavis.edu/
                                                                                                                                                       http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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/dev_stage="1- to 5-days old protoplast"
/clone_lib="HaSemS3"
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clone="HM0007"
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/cultivar="Emil"
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Pred. No. 1
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Mismatches 132;
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RESULT 11
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German Genome Project.

No s1 sequence available.

No s1 sequence available at the RZPD in Berlin.

This clone (DXF2p77972254) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for details.
Plate: QHM3
                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                    Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)

Contact: MIPS
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DKFZp779J2254_5', mRNA sequence.
BX500256
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 437)
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/lab_host="E.coli"
/clone lib="CM M sunflower H.argophyllus"
/clone lib="OH M sunflower H.largophyllus"
/note="Vector: pBRcDNASfiAB; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector. Details of library construction can be obtained at http://cgpdb.ucdavis.edu/"
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/clone="QHM3P22"
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Location/Qualifiers
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47.4%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 bp "Lucal" Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 132;
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AUTHORS
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Best Local :
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

1 (bases 1 to 447)

1 (bases 1 to 447)

1 (bases 1 to 447)

2 (Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.

Lettuce and Sumflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
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EST.
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Plate: QHM8 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              belongs to contig OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: akozik@atgc
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/lab_host="E.coli"
/clone lib="OH M sunflower H.argophyllus"
/clone lib="OH M sunflower H.argophyllus"
/note="Vector: pBRcDNASfiAB; The library was constructed
/rom three different sources (seedling, root and leaf) of
RNA from a single genotype. cDNAs were pooled and
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/tissue_type="liver"
/dev_stage="fetal"
/lab_host="UH10B"
/clome_lib="779 (synonym: hnccl)"
/note="Vector: pSportl_Sfi; Site_1: SfiIA; Site_2: SfiIB"
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                                                                                                                                                                                                                   /organism="Helianthus argophyllus"
/mol_type="mRNN"
/db_xref="taxon:73275"
/clone="QHM8F22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     org [michelmore@vegmail.ucdavis.edu]
)H_CA_Contig2435_2, see http://cgpdb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.6; DB
Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see http://cgpdb.ucdavis.edu/
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Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Z
Lai, Z., Church, S., Jackson, L. and Bradford, K. Z
Lettuce and Sunflower ESTs from the Compositae Genome P
http://compgenomics.ucdavis.edu/
Unpublished (2002)
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QHM3J13.yg.ab1 QH M sunflower H. CDNA clone QHM3J13, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
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                                                                                                                                                                                                                                                                 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2435_2, see http://cgpdb.
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Location/Qualifiers
/clone lib="QH_M sunflower H.argophyllus"
/note="Vector: pBRcDNASfiAB; The library was constructed
from three different sources (seedling, root and leaf) of
RNA from a single genotype. cDNAs were pooled and
                                                                                                     /db_xref="taxon:73275"
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argophyllus Helianthus argophyllus.
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CF096847.1
                                                                                                                                                                                                                                                                                                                                                  Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Ries Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Z Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome P
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QHNZF11.yg.ab1 QH_N sunflower H.argophyllus (drought stre
Helianthus argophyllus cDNA clone QHNZF11, mRNA sequence-
                                                                                                                                                                                                                                                                 Email: akozik@atgc.org [michelmore@vebelongs to contig QH_CA_Contig2435_2,
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Helianthus argophyllus
                                                                                                                                                                                                                             Plate: QHN2
                                                                                                                                                                                                                                                                                                             Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://compgenomics.ucdavis.edu/
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/lab_host="E.coli"
/clone lib="QH N sunflower H.argophyllus (drought stress)"
/clone lib="QH N sunflower H.argophyllus (drought stress)"
/note="Vector: pGEM-T; The library was constructed from
three different sources (seedling, root and leaf) of RNA
from a single genotype. cDNAs were pooled and cloned into
                                                                                                                        /organism="Helianthus argophyllus"
/mol_type="mRNA"
/db_xref="taxon:73275"
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                                                                                                         clone="QHN2F11"
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Pred. No. 1
                                                                                                                                                                                                                                                                                       [michelmore@vegmail.ucdavis.edu]
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                                                                          114;
                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
Contact: Tamborindeguy C
Contact: Tamborindeguy C
Laboratcire de Biotechnologie et Amelioration des Plantes
Laboratcire de Biotechnologie et Toulouse - Ecole National
Superieure Agronomique de Toulouse
Superieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOUGEAN 31326, France.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AAGGTAAAACTTCGTCGCCAGAGCTAGTCGGGGAAGAAGGAGATTGTGCTGTAAACATAA 124
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnollophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

1 (bases 1 to 451)

1 (bases 3 to 451)
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AJ540178 HaSemS3 Helianthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helianthus annuus (common sunflower)
                                                                                               Similarity
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                                 TIGATOTICATACTITACTOAAAGAAGAAATGCCGCTGGCTTTTGATCATGTCGCGCAAA 517
TAGATACACACATCTAAATCACAAAGGAGGTGGCCCCAGTATGTGAACAAGTCCAACAAG
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ilarity 46.5%;
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                                                                                                                                                                 /tissue_type="hypocotyl"
/cell_type="protoplast"
/dev_stage="1- to 5-days old protoplast"
/clone_lib="HaSemS3"
                                                                                                                                                                                                                                                                                           /organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="Emil"
                                                                                                                                                                                                                                                 db_xref="taxon:4232"
clone="HM0013"
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TATACATTIGCGATAGAGTICTIGTGTGGGGTGAACAAAGAGGGGGATTGTCGTGAGTACC
                                                                           AAAAGGAAAACGCGAAGGTTAATGCGCAAACTATCGCAGAAGGAACCAGCATCCCCGAGA
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Search completed: April 30, 2004, 18:35:03 Job time: 2273.3 secs

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Match Length
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1: /ggn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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                                                                                 sequence 286, Appli sequence 5, Appli sequence 1803), A sequence 1, Appli sequence 1, Appli sequence 10, Appli sequence 1134, Appli sequence 2142, Appli sequence 2144, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 5, Appli sequence 91, Appli sequen
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                             sequence
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APPLICATION UNMEER: US/09/107,532A

FILING DATA:
APPLICATION UNMEER: 60/085,598

PRIOR APPLICATION NUMEER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMEER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMEER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEPHONE: (781)893-507

TELEPAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 286:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 base pairs
                                                                    FEATURE:
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28 31.4 3.9 2758 4 US-09-221-017B-441 29 31.2 3.9 2290 4 US-09-620.31D-891 30 31 3.9 477 4 US-09-489-039A-801 31 3.9 1089 4 US-09-134-000C-901 31 3.9 1648 4 US-09-543-681A-3313 33 30.8 3.9 1152 4 US-09-540-236-1145 34 30.8 3.9 1152 4 US-09-540-002-40 35 30.6 3.8 500 3 US-09-2479-19 36 30.6 3.8 678 3 US-09-232-479-19 37 30.6 3.8 678 4 US-09-232-479-19 38 30.6 3.8 678 4 US-09-784-9901 39 30.6 3.8 678 4 US-09-784-990-19 39 30.6 3.8 2829 3 US-08-851-693A-53 40 30.6 3.8 2829 3 US-08-851-693A-53 41 30.6 3.8 2829 4 US-09-430-323-53 42 30.6 3.8 2829 4 US-09-430-323-53 43 30.6 3.8 2829 4 US-09-721-456-220 44 30.6 3.8 2829 4 US-09-721-456-220 45 30.6 3.8 2829 4 US-09-721-456-220
2.758 4 US 1.3.9 2790 4 US 1.3.9 1089 4 US 1.3.9 11089 4 US 1.3.9 1152 4 US 1.3.9 1152 4 US 1.3.9 1152 4 US 1.3.9 1251 4 US 1.3.9 1251 4 US 1.3.8 1500 3 US 1.3.8 1500 3 US 1.3.8 2829 3 US 1.3.8 2829 3 US 1.3.8 2829 3 US 1.3.8 2829 4 US 1.3.8 2829
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58 4 US
US-09-221-0178-441 US-09-489-039A-801 US-09-489-039A-801 US-09-134-000C-901 US-09-149-002-26 US-09-540-236-1145 US-09-540-236-1145 US-09-141-000-2 US-09-141-000-2 US-09-141-000-2 US-09-184-990-19 US-09-784-990-19 US-09-784-990-19 US-09-784-990-19 US-09-784-990-19 US-09-784-990-19 US-09-784-990-19 US-09-784-990-19 US-09-194-195-193 US-08-974-549A-220 US-08-974-549A-220 US-09-402-1818-220 US-09-721-456-220 US-09-721-456-220 US-09-721-456-220 US-09-721-456-220 US-09-721-456-220

US-09-107-532A-286

; Sequence 286, Application US/09107532A
; Sequence 286, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; GENERAL INFORMATION: DOUCETTE-Stamm
; MUCLEIC ACID ;
; TITLE OF INVENTION: NUCLEIC ACID ; CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION NUMBER OF SEQUENCES: 7310 100 Beaver Street and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

ALIGNMENTS

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660 CITY: WALLION,
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354 COMPUTER: PC
OPERATING SYSTEM: <Unknown>

TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

NAME/KEY: misc feature LOCATION: (B) LOCATION 1...552

US-08-026-138E-5

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US-08-026-138E-5/c
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                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P-4551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 966-2340
TELEPAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4392 nucleic acids
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APPLICATION NUMBER: JP 39563/1992

FILING DATE: 26-FEB-1992

APPLICATION NUMBER: JP 173155/1992

APPLICATION NUMBER: JP 215017/1992

APPLICATION NUMBER: JP 215017/1992

FILING DATE: 12-AUG-1992

FILING DATE: 12-AUG-1992

APPLICATION NUMBER: JP 303878/1992

FILING DATE: 13-MOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Hamburg, C.Bruce

REGISTRATION NUMBER: 22,389

REGISTRATION NUMBER: 22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Masayo
ORGANISM: mouse
ORGANISM: mouse
TISSUE TYPE: cerebellum
PUBLICATION INFORMATION:
BUBLICATION INFORMATION:
AUTHORS: Massyobh MISHINA
AUTHORS: MASSYOBH AUGHINA
TITLE: NOVZL PROTEINS AND GENES CODING THE SAME
TITLE: RESIDUES IN SEQ ID NO: 5: FROM 1 to 4392
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                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
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                                                                                                                                                                                                                            LENGTH: 4392 nucleic acids
TYPE: nucleic acid
STRANDEDNESS: double strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Niigata-shi
STATE: Niigata-ke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
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5214, Nishiohata-machi
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Pred. No. 0.048;
0; Mismatches 79; Indels
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2920
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US-09-489-039A-2920
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                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                           Sequence 5, Application Patent No. 6372889 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2920
LENGTH: 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2920, Application US/09489039A Patent No. 6610836
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Best Local Similarity
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Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: PNEUVONIAE FOR DIAGNOSTICS A
FILE REFERENCE: 2709.2004001
           FILE REFERENCE: 97-67
CURRENT APPLICATION NUMBER: US/09/294,531B
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 60/082,513
PRIOR FILING DATE: 1998-04-21
                                                                                                     APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: SOLUBLE PROTEIN ZIMPO-1
                                                                                                                       APPLICANT: Sheppard, Paul O.
APPLICANT: Conklin, Darrell C.
APPLICANT: Farrah, Theresa M.
APPLICANT: Mauer, Mark F.
APPLICANT: Grossmann, Angelika
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
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                                                                                                                                                                                                                                                                                                                                                                                                              ACACCAAATATGGCTCGTCATTATCGTCATGACCATTATCGGCGGGGGGGATCGTTACCC 1204
                                                                                                                                                                                                                                                                                                                                            CGGTGATGGGCTTTGTCAGCGACGCCGCCG 1234
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Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D SEQUENCES RELATING TO KLEBSIELLA AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-09-621-976-18033
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18033
LENGTH: 474
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SEQ ID NO 5
LENGTH: 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.2
Best Local Similarity 32.6
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n=a, g, c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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                                                                                                                                                             162
  282
                                      708
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                                                                                                                                                                                                    588
                                                                                                                                                                                                                                      102 KTKSCMAGRWKGKYYYSRWYYYCYKGACYYMWKRWYCSSCCMMYTKGGGSMWTTTWMMRR 161
                                                                                                                                                                                                                                                                             528 GTGGCAAAATTACGCGCTGCGGTTGAATACACATCCGTGGTACTATTTTCATTAGAAAA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 TATCGTCTTGCCAGTCAT 765
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                                                                                                                                                                                                                                                                                                                                             Similarity
  WKGSCMWKRAWWARKTTYYTWAWYYTTYYKRMCCYYMRKTTYCMMMWYSRWWRGSMWTAR 341
                                    CGCATCTTGTAAAGGCAAAGGAGCCAAACCAGCCACCGTTTATCGTCTTGCCAGTCATGA 767
                                                                                                                      CATGACCATTAAACGCCGCTTGATCAATACCGGGGTGATCGTCAGTACCAATAAAATGGC 707
                                                                                                                                                           RKKSYKRWTKGKKKKKTTWMMAAMCYTTWRSYWMMMRRAAAAKTYYYCMMSKTMCCMAC 221
                                                                                                                                                                                                 AGAGTTTTTAGTGGCGGATATTATTGATGCCTACGCCAAATTTGGCGTCGAAGTTAATCG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCCNSWNCCDATNARRIANCKNGGRTINSWCCADATNARRICNSWRAANGTRICYTCYTC
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                                                                             CCMMCCMRRARSCCMRSCMRSTTYMMCYYYYMMYKGGRMYWWWRGGMWKRMYMMYKKKKSM
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32.6%; Pred. No. 0.62;
ative 27; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                         4.2%; Score 33.4; DB 4; Length 474; 12.5%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                      Mismatches 119;
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US-09-643-990A-1
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Sequence 1, Application US/09643990A Patent No. 6528289
GENERAL INFORMATION:
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                  1807182 AGTÄATGCCATCA 1807194
                                                                                                                                                            1807122 ÁACGÁTTTTTTGGTCGCCGTCÁATCTTCÁAGCCGTCGCCAACTTTTTGCTTCGTATTTAAC 1807181
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
STREET: 9410 Key West
                                                                                                                                                                                    586 AAAGAGTTTTTAGTGGCGGATATTATTGATGCCTACGCCAAATTTGGCGTCGAAGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 GAWWCYWYYYMAARKKKYMWWAAAARGGW
                                                                                                                                646 CGCATGACCATTA 658
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                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1830121 base pairs
                                                                                                                                                                                                                4.1%;
nilarity 65.8%;
Conservative 0
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Pred. No.
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APPLICANT: Robert D.

Fleischmann

Mark D. Adams Owen White Hamilton O. Smith

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US-09-489-039A-10/c
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPHONE: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                              Query Match
Best Local
                                                                                                                                                                                                                                                      Sequence 10, Application US/09489039A Patent No. 6610836
LENGTH: 552
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                     1807182 AGTAATGCCATCA 1807194
                                                                                                                                                                                                                                                                                                                                                                                                                                           1807122 AACGATTTTTTGGTCGCCGTCAATCTTCAAGCCGTCGCCAACTTTTTGCTTCGTATTTAAC 1807181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: «Unknown» PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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CORRESPONDENCE ADDRESS: Human G
                                                                                                                                                                                                                                                                                                                                                                                                          646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 AAAGAGTTTTTAGTGGCGGATATTATTGATGCCTACGCCAAATTTGGCGTCGAAGTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key West Avenue
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Pred. No. 52;
0; Mismatches 25; Indels 0;
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PATECHE INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 825
LENGTH: 825
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US-09-134-001C-2442/c
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Best Local Similarity
Matches 59; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                               APPLICANT: Mohr, Christine
APPLICANT: Wendland, Juzgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
                  COUNTRY: U
                                                                   ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 TCCAATCGTTCCAGCTAATACAGCTGTGATGATATCAACCAGA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 CGAAATCTATCCAGGTTTTACTGGTGAAACGCTCTAATCCAAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 TGTTTATTAGGGAAGCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTTGCGC 124
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                      No.
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGAATTCTGGAATAATTGTGCGTGTAGCTTTCGATCTAATATTTCTACTACTAAGTA 529
                                                                                                                                                                                                                                                                                Philippsen, Pete:
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09134001C
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                                                    6239264th Carolina
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; Pred. No. 0.52,
0; Mismatches
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US-08-925-230-2
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08925230 Patent No. 6147194
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                          APPLICANT: COllart, Frank
APPLICANT: Huberman, Elleze
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: AND GME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (go ORIGINAL SOURCE: ORGANISM: PAG1690UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435 ·
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT IMFORMATION:
ATTORNEY/AGENT IMFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                 CITY: Houston
                                                                                                                              COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                           STREET:
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TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-DE
                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 ACTTAGGGGÁGACGACTTCGÁGAAGGGGATAAGÁGGCAAGCGCGAGGGGGCTAGCGCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 AAAAGTCCATACTTATCCTAATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 GGCAACTAGTGCCTGGCGAACGTAGACAGCAGTTTTCGACTAGGAGGTCGCTGGGATCCA 393
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                                                                                                                                                                 Texas
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                                                                                                                                                                                                       E: Arnold, Wh
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1%; Score 32.4; DB 3; Length 696; ilarity 47.5%; Pred. No. 0.71; Conservative 0; Mismatches 106; Indels
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N: 435
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METHODS AND MATERIALS RELATING TO IMPDH
AND GMP PRODUCTION
                                                                                                                                                                                                                               White & Durkee
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RESULT 12
US-09-712-372-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application Patent No. 6479628 GENERAL INFORMATION:
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 5,665,583
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/712,372
PILING DATE: 13-No. 6479628-2000
PRIOR APPLICATION NUMBER: US/08/925,230
PILING DATE: 13-No. 6479628-2000
PRIOR APPLICATION NUMBER: US/08/925,230
PILING DATE: September 8, 1997
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,259
REFERENCED_DOCKET NUMBER: ARCD:274
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huberman, Bliezer
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
AND GMP PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Collart, Frank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
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RESULT 13
US-08-956-171E-444
; Sequence 444, App
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                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-956-171E-444
                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6593114
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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    Matches
                                                                                                                               INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 11466 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
/ Match 4.1%;
Local Similarity 60.0%;
les 54; Conservative
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                                                                                                                                                                                                                     ATTUKNEI/ MAIK J. Hyman

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION IMFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658 AAACGCCGCTTGATCAATACCGGGGTGATCGTCAGTAC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 GTGAGGGATGTTTTTGAAGCCAAAGCCAGGCATGGCTTCTGTGGTATCCCCATCACAGAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGCCGGATGGGGAGTCGACTGGTGGGCATCATTTC 501
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    Score 32.4; DB 4; Length 11466; Pred. No. 4; 0; Mismatches 36; Indels 0;
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Pred. No. 1.
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US-08-212-133A-7/c
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US-09-328-352-4044/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4044
LENGTH: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4044, Appli
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Sequence 7, Application US/08212133A
Patent No. 5663060
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/212,133A
FILING DATE: March 11, 1994
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Kilpatric
                                                                                                                                                                         CITY: Atlanta
STATE: Georgi
                                                                                                                                                       COUNTRY:
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RIGHASSIFICATION: 415

RETURN APPLICATION BORTA, 004

FILING ANTE STATES

ATTORNEY AGENT INFORMATION:

NAME: Pable, Pattes I.

NAME: Pable, Pattes I.

RESISTATION MUNGER: 31,284

RESISTATION MUNGER:
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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798
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            Published Applications NA:*

1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

8: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

10: /cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

12: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

13: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

14: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

15: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

16: /cgn2 6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

17: /cgn2 6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

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10195.950 Million cell updates/sec
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                     US-10-603-260-2
US-10-603-260-1
US-10-603-260-4
US-10-34-143-153
US-10-34-143-153
US-10-142-426-426
US-10-146-731-426
US-10-140-731-426
US-10-140-731-426
US-10-140-731-426
US-10-140-731-761-426
US-10-140-731-761-426
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Sequence 2, Appli
Sequence 1, Appli
Sequence 41398, App
Sequence 413, App
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Sequence 55, Appl	Sequence 8898, Ap	₹D	Sequence 444, App		e 20548	Sequence 6281, Ap	Seguence 24137, A			Sequence 26418, A	Sequence 1, Appli	e 1, A		53712,	1960,	16031,	346,	42179,	92408,	2408,	Sequence 2058, Ap			31683,		1768,	26132	e 426,	Sequence 426, App	-

ALIGNMENTS

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; LOCATION: (1)..(798)
; OTHER INFORMATION: vall1 gene
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CURRENT FILING DATE: 2003-06-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Kopatentin 1.71
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
ORGANISM: Vibrio metschnikovii RH530
ORGANISM: Vibrio metschnikovii RH530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10603260
Publication No. US20040009570A1
GENERAL INFORMATION:
APPLICANT: CJ Corporation
TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and a
TITLE OF INVENTION: nucleotide sequence encoding the same
FILE REFERENCE:
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
121 GCGCCGAAATCTATCCAGGTTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGT
                                                                                                                                                                                                                                      tch 100.0%; Score 798; DB 16; Length 798; al Similarity 100.0%; Pred. No. 1.4e-239; 798; Conservative 0; Mismatches 0; Indels 0
                                                                  61
                                                                                                   61 CCGTTGTTTATTAGGGAAGCCATTATGATTGTCACTATCGATATGATTTGTCTGCGTCTT 120
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Sequence 1, Application US/10603260

; Publication No. US20040009570A1

; GENERAL INFORMATION:
    APPLICANT: CJ Corporation
    TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and
    TITLE OF INVENTION: mucleotide sequence encoding the same
    FILE REFERENCE:
    CURRENT APPLICATION NUMBER: US/10/603,260

; CURRENT FILING DATE: 2003-06-24

NUMBER OF SEQ ID NOS: 5

; SOFTWARE: KopatentIn 1.71

; LENGTH: 2578

TYPE: DNA

ORGANISM: Vibrio metschnikovii RH530
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US-10-603-260-1
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Matches 798
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 ATGTTTGTCACAAAGTCTTATTTACATTTGACCATCATCATGCACTTACCTAAAATAAGC
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US-10-282-122A-41398
; Sequence 41398, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identificat
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: 60/230,335
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                           GTGGTACTATTTCATTAGAAAAAGAGTTTTTAGTGGCGGATATTATTGATGCCTACGCC
                                                                                                                                       CATGTGGCGCAAATTCAGCATGCATGGAAAAAACTGCGCGCAGCGGTTGAGTACACTTCT
                                                                                                                                                                                                                  CGTGTTAATTGGTTTGCACTAGAGACGATTTTTGCAAGGTAAACAAGTTCTGGCGTTTGAT
                                                                                                                                                                                                                                                      CGCGCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATGCCGCTGGCTTTTGAT 504
                                                                                                                                                                                                                                                                                                                                                                          CCTTTGGTGGACGGTAATCCTAAACGCGATCCAAGCGGTTGGAGCATCAGTATTTCTCAC 300
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Pred. No. 1.9
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; ORGANISM: Homo
US-10-334-143-153
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US-10-142-426-426/c
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Publication No. US20040009549A1
GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
                                                                                                                                                                                                                                                                                                                                           Sequence 426, Application US/10142426 Publication No. US20040048333A1
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SEQ ID NO 153
LENGTH: 8202
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Best Local
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
                   APPLICANT:
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I: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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                                                                                                    Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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                   Watanabe, Colin K
Wood, William
Zhang, Zemin
                                                                   Stewart, Timothy A. Tumas, Daniel
                                                                                                                                                                                                                Filvaroff, Ellen
Gao, Wei-Qiang
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Pred. No. 2.4;
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RESULT 6
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                                                                               APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P330R1C224
CURRENT APPLICATION NUMBER: US/10/142,426
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
                                                                                                                                                                                              Sequence 426, Application US/10123155 Publication No. US20030068794A1
                                                                                                                                                                                 GENERAL
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Best Local
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nes 42; Conserv
                                                                                                                                                                                 INFORMATION:
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Deporge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary S.
Goddwaki, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                  Beresini, Maureen
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Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-155-426
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RESULT 7
US-10-146-731-426/c
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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                                                                                         670 ATCAATAC 677
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Wood, William
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Sequence 426, Application US/10146731
Publication No. US20030129692A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: APPLICANT: APPLICANT:

Beresini, Maureen DeForge, Laura Desnoyers, Luc

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US-10-146-731-426
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
TYPE: PRT
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Best Local Similarity
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APPLICANT:
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
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Publication No. US20030138888A1
GENERAL INFORMATION:
APPLICANT: Baker, Keyin P.
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DTN.NN.NMH.D.M.T.MM.T.Y..YSSTAMSBC..SR.H.HACB..TKRB...G...YM
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                                                                                                                                       YG.KYHHCGNBTC.Y., CHB.MT.HYWA.T.HDGDSGC.SR.NB.W., CSNBTTH., YY.
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                                                               .A....HHHR.C.HRYRRNWS.R.CC.NH..CM.CRMHRMMY.H.HM.B.RTYN.M..HC
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Watanabe, Colin K
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Godowski, Paul J.
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DeForge, Laura
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
TYPE: PRT
ORGANICAT
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US-10-141-761-426/c
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US-10-141-761-426
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Best Local Similarity
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                                            YG. KYHHCGNBTC.Y., CHB.MT.HYWA.T.HDGDSGC.SR.NB.W., CSNBTTH., YY.
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Godowski, Paul J.
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Filvaroff, Ellen
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RESULT 10
US-10-142-885-426/c
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CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wraj
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
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les 42; Conser
                                               314 H. ANTS...H.ND.B.R.MTH.SN...KCS.Y.YA.SA.GHCCMSG.A.WC.CT
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               430 GGTATCGACCCCGAGCGCGCTAATTGGTTTGATCTTCATACTTTACTCAAAGAAGAAATG 489
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                     .S...BR.NSG.H.TSSGH.YCB..DHNM..AM.MM...HNSN.NMC.D....WYDDT.Y 315
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Watanabe, Colin K
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Filvaroff, Ellen
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US-10-158-790-426/c
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
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-10-158-790-426
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CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
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4.4%; Score 35; DB 15; Length 74
Local Similarity 7.7%; Pred. No. 5.5;
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                                AATTTTATCAGCGATCCGCTGGTTGATGGCAACCCCAAACGCGATCCGAATGGTTGGAGT 369
                                                                GW.T..HB.W..MHNT..N..C.AABDSNBS.MT.T..HR..MMCDD..R.MAC.CM.BT
                                                                                                  GATGAGGATTTTGATGCAGCGAGACGACGTATTTGTCGGCAAAAAGTCCATACTTATCCT 309
                                                                                                                                DC.R.D.NS.N.BBAA.RT., NRKNG, C.DBAGH.AC.M..CR..NSTYY.....TYG..
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Godowski, Paul J.
Gurney, Austin L.
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BR.NSG.H.TSSGH:YCB..DHNM..AM.MM...HNSN.NMC.D....WYDDT.Y 315
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; TYPE: PRT
; ORGANISM: Homo
US-10-137-871-426
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC153
CURRENT APPLICATION UMMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
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                                                                                    554 YMW..K.B.G.DGW.SR.HBKWB.NDMY.AB..N.AA.A.SBBS.NK.H......TSD
494 DC.R.D.NS.N.BBAA.RT..NRKNG.C.DBAGH.AC.M..CR..NSTYY.....TYG..
                                     190 GCATTGCCTGGCGGGATAGTGTATGACGAAGATATGACCGCTCATGGTGGAGAACCTGTC
                                                                                                                           130 TCTATCCAGGTTTTACTGGTGAAACGCTCTAATCCAAATCGGCCAGATTGTGGTAAATGG 189
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
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Gerritsen, Mary E.
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                                                                                                                                                                      4.4%; Score 35; DB 16; L
llarity 7.7%; Pred. No. 5.5;
Conservative 157; Mismatches 349;
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                                                                                              Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
LENGTH: 747
TYPE: PRT
ORGANISM: Homo Sapien
3-10-140-923-426
                             Query Match
Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/140,923
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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                             4.4%; Score 35; DB: ilarity 7.7%; Pred. No. 5.5; Conservative 157; Mismatches
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                                                 DB 16;
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RESULT 14
US-10-141-756-426/c
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                                      Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 426
1.FNCTTV
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Publication No. US20030207359A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
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ORGANISM: Homo Sapien
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                                                                                                                                                                                               Zhang, Zemin
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Godowski, Paul J.
Gurney, Austin L.
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DeForge, Laura
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Publication No. US20030207361A1
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          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3333R1C197
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APPLICATION NUMBER: US/10/141,759
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                                                                                                                                            Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Wood, William
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SEQ ID NO 426
LENGTH: 747
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.HY.RHHM
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Search completed: April 30, 2004, 23:19:44
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Minimum Maximum
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Pred. No. 8 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AP005349	RESULT 1
1 Chen,C.Y., Wu,K.M., Chang,Y.C., Chang,C.H., Tsai,H.C., Liao,T.L., Liu,Y.M., Chen,H.J., Shen,A.B., Li,J.C., Su,T.L., Shao,C.P.,	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.	Vibrio vulnificus YJ016	Vibrio vulnificus YJ016		AP005349.1 GI:37201329	AP005349 BA000038	section 6/8.	Vibrio vulnificus YJ016 DNA, chromosome II, complete genome,	AP005349 247450 bp DNA linear BCT 04-DEC-2003		

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TITLE
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Comparative Genome Analysis of Vibrio vulnificus, a Marine Pathogen

LL Genome Res. 13, 2577-2587 (2003)

2 (bases 1 to 247450)

25 (Chen,C.Y., Wu,K.M. and Tsai,S.F.

Direct Submission

31 Submitted (29-MAY-2002) Shih Feng Tsai, National Health Research

Institutes, Division of Molecular and Genomic Medicine; 128,

Yen-Chiu-Yuan Road, Sec 2, Taipei, Taiwan 1154, Republic of China

(E-mail:petsai@nhri.org.tw, Tel:886-2-8146-1041,

Fax:886-2-2789-0484)

This sequence was determined by the Sequencing Core of the National

Yang-Ming University Genome Research Center (YMGC;

http://genome.ym.edu.tw).
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9360. .10247
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Yuseong-gu, Daejeon 305-811, South Korea
3 (bases 1 to 302331)
Rhee,J.H., Kim,S.Y., Chung,S.S., Lee,S.E. and Choy,H.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio vulnificus CMCP6
Vibrio vulnificus CMCP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-DEC-2002) Department of Microbiology, Genome Research Center for Enteropathogenic Bacteria, Chonnam National University Medical School, Hak-1-Dong, Dong-Gu, Kwang-Ju 501-746, South Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Characterization and Pathogenic Significance of Vibrio vulnificus Antigens Preferentially Expressed in Septicemic Patients Infect. Immun. 71 (10), 5461-5471 (2003)
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Kim,Y.R., Lee,S.E., Kim,C.M., Kim,S.Y., Shin,E.K., Shin,D.H.,
Chung,S.S., Choy,H.E., Proguiske-Fox,A., Hillman,J.D., Handfield,M.
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Vibrio vulnificus CMCP6
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Jeong, H., Moon, Y.H. and Kim, J.J.
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Tvvmgasfrnigeilelagcdrltiapallaeleaaegevveklvdskgaaerpaamt
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domain, an EAL and a GGDEF domain;
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                                                                                                                                                                                                      contains a membrane
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SGD

cps

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ARGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGT 60

Query Match
Best Local Sim
Matches 339;

Similarity

38.5%;

Score 213.8; DB 1; Pred. No. 2.3e-57; 0; Mismatches 187;

Length Indels

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302331; 3; Gaps

Conservative

gene CDS

gene

SGC

gene

SGD

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QMLVADDVSBQLAAGEBAIFGVMIESHLVEGRQDLVDGKAATYGQSITDACIGWEDTE
TVLRQLANAVAARRAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFYQLAYRFEEK"
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CDS

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PUBMED
REFERENCE
AUTHORS
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AE004352/c
LOCUS
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AUTHORS
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ORGANISM
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                                                                                               TITLE
JOURNAL
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MEDLINE
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Direct Submission
Direct Submission
Submitted (14-JUN-2000) The Institute for Genomic Submitted (14-JUN-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1. .10977
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                                                                                                                                         2 (bases 1 to 10977)
Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.:
Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Peterson, J.D., Umayam, L.A.,
Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Vill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,
Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R.,
Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 10977)
Heidelberg, J. F., Elsen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, I. Bodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Dodson, R.J., Haft, D.H., Richardson, D., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE004352 10977 bp DNA linear BCT 10-
Vibrio cholerae Ol biovar eltor str. N16961 chromosome II,
9 of 93 of the complete chromosome.
AE004352 AE003853
AE004352.1 GI:9657475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae Ol biovar eltor str. N16961
vibrio cholerae Ol biovar eltor str. N16961
Bacteria, Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                              Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                       20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCACGGTGGAGGAGACAAAGATATCAGGTATGACTGACCATGTTTTGA 259965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCACAGTAGAAGAAACCAAAATAGCTGGCATGACAGATCATATCGCGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACCTTTAGGGCTGCGCAGCCTTTTACTGCGCGATCCACTG---GACTCCGATGGTACC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAATATGCATGAGGATGTTTGGGATTTTTCCTCAAAAGCTTGGCAGTATTGCAGGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCAATAAAATTGAGCAATTAGGTTTAGGGGTGGCACTAGGTAATTCAGCAGAATTTGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTGTGAAACCCTCTCCCATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCTTCCATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGAAGAAAAGTTTTTCCAATCCATAGACAAAGCGCTCAGCACGACGACGGGGAATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rragrogacacagrrrgggggarrggrgarcaaacgrrarcragaarcgcgcgcaccg
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     eltor
     str. N16961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCT 10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gwinn, M.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VCA0090"
                                                                                                                                                                                      note="identified
                                                                                                                                                                                                            'gene="VCA0094"
                                                                                                                                                                                                                                                                                                                               translation="MEQPCWLRSVNPITWFKYVNEDERTCLLPVTPSRLAKGLEKVHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="identified
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1204. .1500
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'note="'"
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/strain="N16961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="VCA0092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="conserved hypothetical protein"
protein_id="AAF96005.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MARPKIPRRIECHPPASCFKPNGVPIRQLARVELAPDELEALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="GI:9657477"
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trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
table=11
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db_xref="taxon:243277"
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                                                                                         hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="VCA0098"
/note="sinilar to GB:J05568 SP:P18133 PID:147307 GB:U00096
PID:1651456; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
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AQMQHSVNVANKVLKDSGLDIKVNLAATKEVQYDTQPGLKKSQSEVLDAATPFNRIDP
AFADVEAKRQQVGADMVAIFRYLDVNNSGDYERQPNGSYSISGLAWTVAPSAWKYPQ
NAKKSMYSHSYLNEGGAETFIHELGHRIPGLNHAHBQYRELPHINNGTEUDAYGYGIKG
QFATIMAYPHLFGVGRSYKFSSUNLGCBGAPCGVKDYANSVRAIGLTAPHIAQVYTGT
KPPVDDGNPGDTEPTDNTNNVETIKGPLALPDMKILTLPIVVSAQGSSTAQVALDITH
EYRGDLSIRLFAPDGSYMVLKQANRYDRGQSYNVQFTLNDVDPSAAEGEWRLEIQDHF
GGKLGTLNQPQTTPP"
COMplement (5403. .6119)
/gene="VCA0097"
                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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/translation="MMPRLFSHIIRSLL"
/translation="MMPRLFSHIIRSlux"
/translation="MMPRLFSHIIRS
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VIAPKPAPEIELSIHHHPAVELBSTENRVVNEQEEVQEGEEPRVIEPQNIEQVWLPI 
NPTPELADLKPKSQAVTDIQAIEFENIDQFRVLMAGDSATLPLFNGESIRVLIDEAQT 
QAQGIQTWAQNRETQGGTFPVTFTFGQHSIMGFIGHPQGSIKIEGVGHQAWVXQVPDS 
HGFEHDTQSHDRAH"
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/gene="VCA0097"
                                                                                                                                                                                                                                                                        dfnrhlana ydgvrhdsgcpfrwgdkmi ahyqqlgi dpttklf i fsdgldfdqalelc
byfagrvki s fgigtfl indlanwrnaagvbyrpls i viklaecqgrpvaki sdqpbk
amcedp i flanlkrrfni bldvdali qelrhqkrsprhy i saa"
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/db_xref="GI:9657483"
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4167. .5390
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PID:1742694 PID:1742718; identified by sequence
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7856. .8896
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/db_xref="GI:9657481"
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3426. .4124
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/note="identified by Glimmer2; putative"
                                                                                        /856. .8896
/gene="VCA0099"
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Best Local Similarity
Matches 315; Conserv
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                                             Vibrio parahaemolyticus
Vibrio parahaemolyticus
Bacteria; Proteobacteria;
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'Vibrio parahaemolyticus DNA, AP005088 BA000032
AP005088.1 GI:28809504
Nasu,H.,
                                 Vibrionaceae;
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                                                                                                                                                                                                                                                                     ACAGTAGAAGAAACCAAAATAGCTGGCATGACAGATCATAT 521
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ilarity 60.5%;
Conservative
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/tran=1 table=11
/product="oxidoreductase, G
/protein_id="AAF96013.1"
/db_xref="GI:9657485"
Iida, T.,
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/gene="VCA0100"
/note="similar to GP:7226016; identified by sequence
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QEDWPQIAYFDSAQRLITESDVDLVIITAPNNVHFPLAKLALEHGKHVIVEKPFVTQI
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RQRWREQAQEGGGILFDLAFHLLDQALVLFGLPQSLSADCRWREDDATTIDYFDLQLY
PPQHVVRLHANLYSBFENVRYQVLASLGKYVKYGLDPQEDRLKAGERPFHPQWSQEN
PQYGILYHAEGNENVITELGGYQHYFTQVVEAIRNGASNPVSAESALQSIQLIELALE
                                 Vibrio,
Sugahara, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 191.4; DB 1;
Pred. No. 2.6e-50;
0; Mismatches 206;
                                               Gammaproteobacteria;
                                                                                                                                             bp DNA chromosome
   Yamaichi,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gfo/Idh/MocA family"
                                                                                                                                             'n
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                                                                                                                                                           linear
     Park, K.S.,
                                                    Vibrionales;
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                                                                                                                                            sequence,
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     Yokoyama, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Makino,K., Shinagawa,H. and Honda,T.
A filamentous phage associated with recent pandemic Vibrio parahaemolyticus 03:K6 strains
J. Clin. Microbiol. 38 (6), 2156-2161 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V cholerae Lancet 361 (9359), 743-749 (2003)
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                                                                                                                                                                                                                              /codon_start=1
/evidence=not=1n
/transl_table=11
/product="cytochrome BD2, start="bp-start=1" bp-start=1" bp-start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cytochrome BD2, subunit I"
/protein_id="BAC62480.1"
/protein_id="BAC62480.1"
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/db xref="Gd1:28809505"
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/rubbyoktyHwskifayunfcdwscoglwarvoffitwsgfspapestrypLtyEv
/rapplagetvorLigemrvoffithifpatrychaffitsfyiLasuswmoyrogyz
LIAFFLAGELOVALGOMRRVOFFITHIFPATRIAAHHLLRGNQSTAVKT
IVDGRVVPTDWFAIVFNPSFFYRLAHMSVAAFVSSALFVGASAAWHLLRGNQSTAVKT
NFSMSIGILVFLAEIFVLGAVIGDVHGLNTLEHOPAKIAAIEGHNNDSDGKFTPLILEGMP
NMEQRRTVPALEIFVLGAVIGDVHGLNTLEHOPAKIAAIEGHNNDSDGKFTPLILEGMP
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NMEDRRTVALEIFVLGAVIGDVHGLNTLEHOPAKIAAIEGHNDSDGKFTPLILEGMP
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FREKALENHLKEWDRSETVOGSILTFEFGGIVGAVICGFTUENKVEVGALIALIFEGVAFE
IFCGLGLVATYALLGSTWLIMKTEGALQNTMYRFTUKTLLAMISALIIVSAWTFIAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKTRDAVSAHGDLQMSISLLCFLVVYSLVFGFGYYYMIHQIKKGPDAIEHDEHDMTTV
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identity 76 in 437 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sub_strain="RIMD 2210633"
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/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to GB:AAL19315.1 (AE008712) percent dentity 67 in 336 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     evidence=not_experimental/transl_table=11
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Gene="VPA1138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="VPA1138"
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|mol_type="genomic DNA"
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Nakano, M., Yamashita, A.,
Honda, T., Shinagawa, H.,
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4561. .5874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3970. .4326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VPA1140"
complement(2684.
/gene="VPA1140"
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SIWPNIIPPSISIWEAAAPASSQRFMLVGAVIIIPIILAYTFWSYYVFSGKVKEDEAY
/evidence=not_experimental
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                                                                                           /gene="VPA1143"
/note="similar to |
identity 45 in 406
                                                                                                                                                                                                                                      KRLEEKINLYKSGKVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:AAK76923.1 (AE001438) percent
identity 48 in 109 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VPA1141"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
/protein_id="BAC62483.1"
/db_xref="GI:28809508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:AAF96301.1 (AE004375) percent
identity 62 in 250 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2469
                                                                            codon start=1
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dentity 47 in 118 aa"
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/transl_table=11
/product="hypothetical pro
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                                                                                                                                                         ACCACCAGCTTAATCTCTCATGTTGTCGCTATCGGTTCACCTCTTAAAGGCGCGTCCATA
                                                                                                                                                                                                            TCCTGTGAAACCCTCTCCCATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCTTCCATT
                                                                                                                                                                                                                                                                 CTCGTGGGGCACAGCTTGGGAGGCTTGATGATTAAGCGCTATCTCGCCAACAGAAAACCA
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TTAAAAGAACACGACGAATCCCGCTATCCACAAAATCAGGCAGTATTGCAGGAACG
                                                     GTAGGTCGGATTCAAGATCTCGGATTGGGTGCAATTTTAGGAAACTCACCACATCACGGA
                                                                                                    GTCAATAAAATTGAGCAATTAGGTTTAGGGGTGGCACTAGGTAATTCAGCAGAATTTGGG
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5918. .6580
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LNDDVTPTRRHFIRNNGIPPTDVNPETTVTLTIGLVDKPMSLSIADLKKNFDVVEQQL
VVECGGIGRAFFDPKAGGNQWTYGAFATVERTSTYRLADVKAGGVKDGAIYTAHYGAD
KHLSGKEGKLPISRGVPIAKAMGSENLIAFAQNGEALHPMNGAPLRLVVPGWPEGSCGA
KMLTRIQIRDQIHDGPKMTGTSYRVPNRPVAPGENVAKEDFEIIERMPVKSLITSPQT
NTEVNGNEIAIRGHAWSGDRKVTKVQISIDFGATWMDADLAAPANDGAWQTFNAKVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
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/db xref="G1:28809513"
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/translation="MKIMSKCNVFVVSLFTLGLLGCASTKDNMVAKGFPVQYAEGFDD
GCHSGYAAGGSLFDEFKKDLSRFNSDKKYAQGHSDGFRQCESEQEALERQTRITIEQQ
KLIEGRKANEBSETYLLEKHALEGVDTSGLESLTPK"
complement (7370...7972)
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achQfepngvtvvgpplmglaerniaspegfnysdgirqhqgkwdaekldaflsapnd
faQgtnmvfpgvtdpgaraaiiawlatknptppnwnwtssglevkspgdgiltpgenm
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/transl_table=11
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/note="similar to GB:AAG07974.1 (AE004872) percent
identity 48 in 93 aa"
/codon_start=1
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/protein_id="BAC62487.1"
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/transl_table=11
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|dentity 39 in 109 aa"
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/db_xref="GI:28809511"
/translation="MSENEKNKPQGIYKYYENNPKSADEKVFGRVSYPDRRGFLKGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="VPA1144"
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Pred. No. 5.6e-46;
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Best Local
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182
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-JUL-1998) Fallarino A., Dept. of Microbiology and Immunology, University of Adelaide, SA 5005, Adelaide, AUSTRALIA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fallarino, A. Unpublished
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                                GAAACCAAAATAGCTGGCATGACAGATCATAT
                                                              GGATTTCGCCCAATCTTACTCGGTGGCTCAGGAATGTGTGATGGCACGGTCACGGTTGCC 181
                                                                                              GGGCTGCGCAGCCTTTTACTGCGCGATCCACTGGACTCCGATGGTACCGTCACAGTAGAA 489
                                                                                                                                CATCAAGATAGCTGGGAATTGCCACAACGGCTGGGTTGCATTGCAGGAACATTGCGTTTC
                                                                                                                                                            CACGACGACGAATCCCGCTATCCACAAAAATCAGGCAGTATTGCAGGAACGATACCTTTA
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/transT_table=11
/protein_id="CAA13122.1"
/protein_id="CAA13122.1"
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CDGTVTVAETQISGMTDHLLLHQSHTGLVYSHKTARQIDYFIRHNQFQHKKIPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Vibrio cholerae"
/mol_type="genomic DNA"
/strain="Z17561"
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                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukigalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chargel, Chargel, M., Cole, P., Dehrellano, K., Dear, K., Diar, J.S., Dodge, S., Cook, A., Cooke, P., Dehrellano, K., Dewar, K., Diar, J.S., Dodge, S., Farro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Johnson, R., Jones, C., Kamat, A., Katatas, A., Kells, C., Labocque, K., Limazares, R., Landers, T., Lehocky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Maddonald, P., Major, J., Mayvis, N., Mercen, C., Koarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Helmaga, V., Muphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Peter, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Kiley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stenass, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sterauss, N., Wilson, B., Wi, K., Wigner, S., Schupback, R., Schoman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sterauss, N., Wilson, B., Nu, K., Wyann, D., Ye, H.J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submitted (19-70H-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charlee Street, Cambridge, MA 02141, USA (1983) (Charlees Street, Cambridge, MA 02141, USA (1983) (Charlees Street, Cambridge, MA 02141, USA (1983) (Charlees St., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galgan, J., Gardyna, S., Graham, L., Gardyna, S., Graham, L., Gardyna, S., Graham, L., Gardyna, S., Faros, S., Ferreira, M., Hafes, N., Halles, N., MacLean, C., MacCan, J., MacCan, R., MacCan, R., MacCan, R., Cooke, P., Corum, B., Dahrellano, K., MacCan, J., Randers, T., Dehre, C., MacCan, M., MacCan, R., MacCan, R., Cooke, P., Corum, B
                                                                                                                                                                                       On Mar 27, 2003 this sequence version replaced gi:28630062. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                   Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Birren, B., Nusbaum, C.
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC124052
178879 bp DNA linear HTG
Mus musculus clone RP24-440120, WORKING DRAFT SEQUENCE,
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 178879)
                       Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Lander, E.
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NCE, 38
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NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 440 I 20
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of read
Assembly program: Phrap; version 0.960731
Consensus quality: 16751 bases at least Q40
Consensus quality: 173712 bases at least Q20
Consensus quality: 173712 bases at least Q20
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Insert size: 175179; sum-of-contigs
Quality coverage: 5.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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    Project Information

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6: gap of 100 bp
7: contig of 661 bp in length
7: gap of 100 bp
6: contig of 689 bp in length
6: gap of 100 bp
3: contig of 647 bp in length
3: gap of 100 bp
6: gap of 100 bp
6: contig of 670 bp in length
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RESULT 7
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                                                                                                           GATGGCACCGTGGCGCTGGATGAGACGCAGTTGCCGGGGCTGGCCGACCACTGCGTGATC 17618
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/mol type="genomic DNA"
/db xref="taxon:10090"
/clone="RP24-440120"
                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
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31798: contig of 4950 bp in length
31898: gap of 100 bp
37738: contig of 5840 bp in length
37838: gap of 100 bp
52769: contig of 14931 bp in length
52869: gap of 100 bp
65311: contig of 1242 bp in length
65411: gap of 100 bp
74093: contig of 8682 bp in length
674193: gap of 100 bp
94582: contig of 20389 bp in length
94682: gap of 100 bp
134219: contig of 39537 bp in length
134319: gap of 100 bp
134219: contig of 44560 bp in length
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SOURCE

synthetic construct

AX251505 Sequence 473 from Patent AX251505 AX251505.1 GI:15984928

473 from Patent

26997 bp 1t WO0168912.

DNA

linear

PAT 05-OCT-2001

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                                                                                                                                                                                                                                                                                                                                                 390 TCCACAAAATCAGGCAGTATTGCAGGAACGATACCTTTAGGGGCTGCGCAGCCTTTTACT
                                                                                                                                                                                                                                                                                                                                                                                      823 AAWWAKTKYRMGMTGAKTRGRARKARYWWKWATWCATKRWMTKGKGAKWAWTWMAKAWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   763 RYATRIMIMIMYRYSMKWYTWCTIMIGYWWYWRTYMKWRYMWYKCTKTYWYWSATYWTGTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATTGAGCAATTAGGTTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 RSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWKMWR 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GATCAAACGTTATCTAGAATCGCGCGCACCGTCCTGTGAAACCCCTCTCCCCATGTCGTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 TCAAACCATTAGCTACAACTCACTCGCTATCGATGATGAGGCCATTTTTCGCCGCCTTGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TATGCATGGCTTGGTAATGCATCCGCTTAGTCATCGTCTGCATAAATTGGGTTATCGTAC
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. a Plant genes involved in defense against pathogens Patent: WO 03000898-A 5263 03-JAN-2003; Syngenta Participations AG (CH) Incation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX655393 2000 bp DNA Sequence 5263 from Patent WO03000898. AX655393
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                                                                                                                                                                                                                                         WYWYCTTWKMACGRATKYMCCAGWWAMYSYSWTRTYWMRTWRWMWASSRTAKRMARMMWK 1002
                                                                                                                                                                                                                                                                          GCGCGATCCACTGGACTCCGATGGTACCGTCACAGTAGAAGAAACCAAAATAGCTGGCAT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRMSRWKSTTCYWRKWGSMKSTCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWYYYRY
                                                                                                                                                                                                    GACAGATCATATCGCGATATCCAC 533
                                                                                                                                                                                                                                                                                                                  GGTGGCACTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGAATCCCGCTA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 37.2; DB 6; ilarity 7.7%; Pred. No. 2.7; Conservative 231; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-UUI-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL592225

183397 bp DNA linear ROD Mouse DNA sequence from clone RP23-278M14 on chromosome
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                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                   Center code: SC
                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                               On Jul 8, 2002 this sequence version replaced gi:21615572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epigenomics AG (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMATCAGGCAGTATTGCAGGAACGATACCTTTAGGGCTGCGCAGCCTTTTACTGCGCGAT 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCCATCGAAACTAACAATCCATAATACAAATTAAACACTAAATACACGTTAATTTC 13357
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/db xref="taxon:32630"
/note="rhem:----
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1. .26997
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Pred. No. 5.6;
0; Mismatches 127;
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1, complete
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                                                                          RS Birra, B. Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Commarata, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nyuyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefay, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Pieter, N., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC130676.3 GI:28894622
HTG; HTGS_PHASE1; HTGS_DRA
Mus musculus (house mouse)
Submitted (13-AUG-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 209061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC130676 209061 bp
Mus musculus clone RP23-167L15,
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="l"
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/clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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8: Gontig of 6074 bp in length
8: gap of 100 bp
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133912: gap of 100 bp
159643: contig of 25731 bp in length
159743: gap of 100 bp
205188: gap of 100 bp
205288: gap of 100 bp
209061: contig of 3773 bp in length
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COMPANY	TITLE	TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Medlarin, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Medlarin, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nyuyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Feterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission 2 Submitted (19-SBP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA, 02141, USA	Camartat, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacChan, C., MacConald, P., Major, J., Menga, V., Murphy, T., NayLor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., McCarthy, M., Meldrim, J., Nereus, L., Mihova, T., Mlenga, V., Murphy, T., NayLor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L. Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Street, Cambridge, MA 02141, USA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 54762) Birren,B., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone RP13-572F7 Unpublished 2 (bases 1 to 54762) Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barria,N. Rastian V. Bloom T. Bornslaubiv I. Boukhoalter,R.,
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                          gene
                                                                                        misc_feature
                                                                                                                                                                                                                         H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ttp://ncbi.nlm.nih.gov/blast/db) and the cDNA
database, nr (ttp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDNJ. Protein homologies of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP, ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
a probable 'hypothetical' protein and is included as a
miscellaneous feature of the sequence.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone. This sequence of 001793 E31 clone has an overlap with
OSJNBa0036M16 (DDBJ: AP005303) clone at 5' end and with 031657 A07
(DDBJ: AP003930) at 3' end. The sequence was generated by combining
Monsanto and RGP-Japan sequencing data. Detailed information on
overlap and assembly quality together with annotation of this entry
is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

On Aug 21, 2002 this sequence version replaced gi:14595195.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.hmm

(http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor

(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://bioin.cse.psu.edu/html/docs/sim4.html), RaceHMM

(http://gl.bbin.cse.psu.edu/html/docs/sim4.html), RACEHMM

(http://gl.bbin.cse.psu.edu/html/docs/sim4.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlap and assembly is available at
           complement (3384..8953)
/gene="031793 E11.101"
complement (3384..8953)
/gene="031793 E11.101"
/note="probably inactive due to including stop codon(s)
CDS
                                                                                                                                                                         /gene="0J1793_E11.101"
complement(1._.1396)
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                                                                                                                                                                                                                                                                                                                                                          organism="Oryza sativa (japonica cultivar-group)"

"col type="genomic DNA"

"cultivar="Nipponbare"

"db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                    clone="0J1793_E11"
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VPAIFGSFRTAIKDIEYQGYHIPKGWQIFTDQIVTHLDTNFFDGPRKFDPARFHNQSS
IPPYCFVPFGGGPRMCPGNEFAKTGTLVAMHYLVRQFRWKLCCKBEGYRKDPTPMPLL
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FFGBEAGPIREALATDFEALVKATLSIPVNIPFTKFNKGLSASWRIRKLLSRIAYETT
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/gene="001793 E11.104"

join(<21958 .22287,22350 .2

23102 .23287,23433 .>23753)

/gene="001793_E11.104"

/gene="001793_E11.104"
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/gene="0J1793_E11.103"
/5949. .17980
/gene="0J1793_E11.103"
/note="probably inactive due to internal
CDS
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Leaamerargdgmatatarqwwraarggtrrrrrgrgdkwytatggdgdggaaagddg
Dgarrlatwatargdgdkergkeeelg"
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OSJNBa0081P02.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="start and end point are not identified"
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join(25876. .26358,26486. .26924,27017. .27204,27366. .27683)

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/codon_start=1
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join(<25876. .26358,26486.
27366. .>27683)
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/note="start and end point are not identified"
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<11996. .>12388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 CTCGCTATCGATGATGAGGCCATTTTTCGCCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 CCGCTTAGTCATCGTCTGCATAAATTGGGTTATCGTACTCAAACCATTAGCTACAACTCA 111
                                                                                                                                                                                                  271370 bp
Rattus norvegicus clone CH230-71F9,
3 unordered pieces.
AC112046
                                                       AC112046.3 GI:23270281
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTATATTTTGAGGCGGTCATTTACTCCG 77638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTTAAGGGTCCGCTTGCAAAAATAGATTTTCGTAGGCAGACAACGAGCTTCACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5%;
ilarity 62.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (36390. .39069)

/gene="0J1793 E11.107"

/gene="0J1793 E11.107"

/note="probably inactive due to 5' exon missing in CDS probably inactive due to including frameshift(s) in CDS pseudgene, gag/pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="011793_E11.110"

join(<43397. .43891,43997.

44875. .>45180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(joIn(41589. .41794,41957. .42017))
/gene="OJ1793_E11.109"
/note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this category is not included in IRGSP standard" complement (join(41589. .41794,41957. .42017)) /gene="001793_E11.109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSLFGSPTVLLAGPGANHFVFSNQDLIFTETKAINALVGRSILT LSGEELKQVRGALHGYLREEMVTKYNRKMDEEVRRHIDLNMVGHKTVTVVAFLARRLAF DIICSVIFGQGVGFIREALAADFETMVKAMLEIPVNIPFTKFNKGLNASRRIRVLRQ IARDMEGALQQGYSSSADDFTTYMLVLRSKGTHSLTVDDVJUNAIVLLAGRETISSVLITFLIRCLAGEPDIFGKITDEQEELARSKGENEFLTWDDVSRWKYTWKVALEILRTIS PIFGSFRTAIKDIEVRGYHFKGWQVFHAQSITHLDGKFFNDPIKFDFTRFDNQSLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIBLETRTPPEYAHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYCFVPFGGGPSMCPGNEFPRTETLVAMHYLVRQFRWKLCCKEEGYRKDPLPTPVLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="putative 5-alpha-taxadienol-10-beta-hydroxylase"
'protein_id="BAC79651.1"
db_xref="GI;33146518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="OJ1793_E11.106"
/note="contains full-length cDNA(s): AK073618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         category is not included 7. .45180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 8;
Pred. No. 13;
                                                                                                                                                                                                                                                          DNA linear HTG 10-OCT-2002
, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .44435,44534. .44721,
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in CDS

mRNA gene

gene

SgS

LIR

SgS

SdD

m.R.N.A

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allen,C., Allen,H., Alsbrocks,S., Maina,A., Angliano,D.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavacos,I., Ceasar,H., Center,A., Chu,J.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Davila,M., Lscotto,M., Bugen,C., Dunn,M., Durbin,K., Duval,B., Baves,K.,
Egan,A., Escotto,M., Bugen,C., Evans,C.A., Falls,T., Fan,G.,
Errsecr,C.M., Gabial,A., Ganta,R., Garcia,A., Garner,T., Garca,M.,
Genravathe,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Errsecr,C.M., Gabial,A., Ganta,R., Garcia,A., Garner,T., Garca,M.,
Gharvay,Y., Havlak,P., Hawes,A., Hederson,N., Hernandez,J.,
Harvey,Y., Havlak,P., Hawes,A., Hederson,N., Hernandez,J.,
Harvey,Y., Havlak,P., Hawes,A., Hederson,N., Hernandez,J.,
Harvey,Y., Havlak,P., Hawes,A., Hodgson,A., Hogues,M.,
Hernandez,S., Filly,S., Kelly,S., Soctt,G., Shamkord,M., Nathyy,M., Mair,L.,
Nanders
Submitted (10-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 23, 2002 this sequence version replaced gi:21737475.
On Sep 23, 2002 this sequence version replaced gi:21737475.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 271370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 271370)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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RESULT 14
CEW06A7
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                           19579 ACAAGGTTCAGGGGTCGTACTAAGTAATTCAGCTGTGTGCGGTCTACA 19532
                                                                                                                                                                                                                                                                                                                                                              19639 CCGGGTAGTCGGGAACGTATAAAGCTGGCCAGCACCTTCAATAACAGTGCTTGAAGAGAA 19580
                                                                                                                                                                                                                                                                                                                                                                                                                258 CCATGICGICGCCATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATTGAGCA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may extend beyond the ends of the clone and there may be sequence contige within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequences will be indicated in the feature
CEW06A7 27243 bp DNA linear INCaenorhabditis elegans cosmid W06A7, complete sequence Z78066 Z78066.1 GI:1487930 HTG; Histone H4 like. Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                            ATTAGGTTTAGGGGTGGCACTAGGTAATTCAGCAGAATTTTGGGTTAAA 365
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Center clone name: GPPD

Center clone name: GP20-71F9

Center clone name: GP20-71F9

Center clone name: GP20-71F9

Assembly program: Phrap, version 0.990329

Assembly program: Phrap, version 1.990329

Consensus quality: 196607 bases at least Q40

Consensus quality: 192016 bases at least Q20

Consensus quality: 19209 bases at least Q20

Estimated insert size: 199140; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor
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48462
68180
68280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%;
llarity 58.3%;
Conservative
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48462. .50098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10116"
/clone="CH230-71F9"
18147. .19710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_contig"
68280. .70194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_contig"
58905. .60802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48361: contig of 48361 bp in length
48461: gap of unknown length
68179: contig of 19718 bp in length
68279: gap of unknown length
271370: contig of 203091 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Length 271370; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                    linear INV 10-DEC-2003
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FEATURES
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TITLE
JOURNAL
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MEDLINE
REMARK
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TITLE
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                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=W06A?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions.

The true left end of clone W06A7 is at 1 in this sequence. The true right end of clone W06A7 is at 9975 in sequence 278067.

The true left end of clone ZC412 is at 27138 in this sequence. The true right end of clone C48G7 is at 10917 in this sequence. The true right end of clone C48G7 is at 10917 in this sequence. The true right end of clone C48G7 is at 10917 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone W06A7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-AUG-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@anger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     none.
Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                          JUIN (4610. 4719,4772. 4870,5394. 6067. 6106)
                                                                                     complement (9699. .9803)
/gene="W06A7.5"
                                                                                                                                               /translation="MVKIVTDGDYVPWYSRRAPPVPCFPCLPAYMGIWPARKCVLIIG
ALLFFPVIILLAMLITCIAIECAGVASALIPLALILIIVGILLFHCGYAAHLLDNHG
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                                                                                                                                                                                                                                                        /gene="W06A7.2"
/standard_name="W06A7.2"
/codon_start=1
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/protein_id="CAB01521.1"
/db_xref="GI.3880493"
                               complement (9699. .9803)
/gene="W06A7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(4610.
/gene="W06A7.5"
/standard_name="W06A7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="W06A7.2"
join(4610. .471)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:6239"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic D
/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="W06A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1(4610. .4719,4772. .4870,5394. .5604,5655.
1. .6106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5604,5655.
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FTPLDELEPQOKILNEKAEHIEIEASGDĒFIKDHPFPVENEQNVNEQSSRVETVHSFI
GLESSGVGLIGAVSDSVANNYKENTESPDIISLEASGDELSKLVEAREIITESKDAYS
TDVPESRKTYSDUIGLEEAGDKIUSNNYKENTESPDIISLEKKLVEAREIITESKDAYS
TDVPESRKTYSDUIGLEEAGDKIUSNNYKENTESPDISGLALEGALDVPELLPIENSEQ
ETVAVKATESCDHVVDSQKTLERASSLEEDIMSPEVLGITSSQTLSDYLPVISEDQDS
IPPVTEVEETSEKLVKASSLEEDVVSPEVLELDDRVQNKNPESSEVTAVDASKTEGOF
SDSPDSRATETFMEKLVTVTENLLPAGDKLSEERIQEIRENTISGPGKEEDDLENAN
DPDDETIVEXIVSNAESSLFIEAVISTBDGGTSDQPAQNAIDSSETTVDDSQTEEIF
TDDNVKKSKENTPKAENDTEINYLPGGEEGPEDNAEKRNEAVSPNDETSBIKQDLENL
ENGASGDDNNVQVDEAAQEDPTDFETVDETVSKISENREAVSPNDETSBIKQDLENL
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TTEAFFGAAGTOTSDANIEKVAMADEFLPUDELVSIERFPEVKAPASSTGEDDLFR
RDRRTVSLITGTGDQNAPIQVIFVGDGSBIANATQERTSEHNELIESDKESEEAITK
NEEDVDQDFQSEBFLTSQBGEGSSIGNKIVAVVGSVLLGAVIFYGVLASNENEDAHA
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NEEDVDQDFD GSEBFLTSQBGEGSSIGNKIVAVVGSVLLGAVIFYGVLASNENEDAHA
                                                                                                                          NABSHIDQETGGASBIKDDQNQPEEFSAEHQGKFEVSAEPDQESAEFQLEAKKDQDKE
TIENGSDAKKETVMEKLVSLVENILEVEAVLPSDSTVTKNSEDKKELETQELSSKEIL
TSGQPEVVPETSEAFVSDPEIFQRVKRASSTSPKTQKTEPHAPIFIVGGSTEDDESGI
ANVIDELVHEDDEKKVPEVTANISUSASENIDDSTTANAVPKTEVSSBQLQVATVEFE
LESAPEEESAALPEVQEPLEKVEVQPDLSQNSPAPHKIIDLHFNIPKDHEDYGNDYVP
FGTESSEESQKADGNQENGEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVGCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLEDHLSETBEKQNEVESSIKSEKNVIGLEDSGDTFRDTSGLAPAEDNEAEATITTDF
VPLESAGDIPSENEIKEVASAPDVVGLEEYIIGNIPNAPVVNDDIPNVFTPEVANDET
VETFSVTAEEASIPVVVELEPIGDEYEFQRPVENFSEPSDNINLEESGAEQVLLENNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFYFREISGRRNLLLLGTAYGFTLFGYTVITASRVVQL.

complement (join(12347. .12413,12490. .12861,12918. .13068, 13512. .13590,14170. .14538,16386. .16466,16510. .17323, 19088. .19168,20833. .21123,21182. .21300,21521. .26999))
/gene="ret-1"
                                                                                                                                                                                                                                                                                                                                                                                              DREVZETGDSTRDRPZEETFVSKLTSMVENILPSTNDENPEAVSMVENVLPVNTEGLD
ESKEDNPDAPTAEAHSGEKNLRNDKTTDTRERDPEETILNKLVENALPTGVTGSFTE
VSAPDAQELDETVVDHAGQNDTSEVEDAPEKSAGGTVIEKFTSNIESILPVQAPTQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /txanslation="meapavigledsgdninrpaletasdgessenkepdasenveet
epvssakvialessgdceegnikisanensvepdgadkpahtegeiptiilpsettvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(12347. .12413,12490. .12861,12918. .13068, 16386. .16466,16510. .17323,19088. .19168,20833. .21123, 21182. .21300,21521. .26999))
                                          DVDASDVNEQDEESTLKILKVVPSEPSLLELDFTNDPKVIHVPIPLMEPATMYLEEMV
EWIIADAVKEVSEMEVVTESEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGIILLIVGSSIYPFIKVNVVGSVASDTVLPMEKLHQHTQNTEDNVTISYWKKVIAWI
GTVIVGLSLGVMTTPVTLLMTRHDIYPKSSEITSPVSFHFSFFTGVMIVSVIIFIAYC
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join(10078. .10235,10496. .10565,10609. .10746,11390.
,11614. .11806,11854. .11946)
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/db_xref="GI:5596654"
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/standard_name="W06A7.3c"
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/protein_id="CAB01524.2"
/db_xref="GI:15718229"
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cDNA EST CEMSF72F comes from this gene
cDNA EST yk1089h08.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="W06A7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ="C. elegans RET-1 protein (corresponding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        name="W06A7.4"
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gene

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Mus musculus clone sequence. AC069562
AC069562.51
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                                                                                                                                                                                                                                                             AAATCAGGCAGTATTGCAGGAACGATACCTTTAGGGCTGCGCAGCCTTTTACTGC 451
                                                                                                                                                                                                                                                                                                              AATGGAAATATATCTTAACTATAGTTATGAAAATATGACAACGAAAAATCTGAACACAC
                                                                                                                                                                                                                                                                                                                                                               CTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGAATCCCCGCTATCCACAA 396
                                                                                                                                                                                                                                                                                                                                                                                                             TTACATTTTTAAACAATTAAATTTTCAATAATACTGAATTCATAGGTTATCGTATAGTC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACCTTTGCAAGGAGCTTCCATTGTCAATAAATTGAGCAATTAGGTTTAGGGGTGGCA
                                                                                                                                                                                                                   AATTATTAAAGCCTGACACCGAAGACATCAGGAGGCACTTCCATAAATTTTTTGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%;
llarity 50.3%;
Conservative
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14170. .14538,16386. .16466,16510. .17323,19088. .19168,
20833. .21123,21182. .21300,21521. .26999))
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PIAEEARKLVQDAVESASEYKKQAVDSGDBIGRELLDNVEQKIEQVKEPIVDSLHKAY
DGVGDFVHETVPNAVDDFVREAEKQLPESPVPEKIETPEPLVDIHDTVDKVHDEVDNF
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FGDRQKFRTAIENIRQDLLPFQSSVSQYLRSSPNPSQQLLVTNLSMDSPSDLSPNAPP
VGFENTAQFLEKLQQEDRPSAEGSIDSSGFEKVDHEGLDEFAAPPVHDFMQKSVFGSL
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epvssakvialessgdceegnikisanensvepdgadkpahteqeiptiilpsettvt
qledhlseteekqnevessikseknvigledsgdtfrdtsglapaedneaeatittdp
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LDDFDPLVTSNTGAAFGAAVGAAAAVESLTEEEMFGHQKFETVPRPPTPPKOISDEDV
KPSTVNLGPSHHHSHPSSPHHSILKHHGDAWIDFKTVPPCVLDVIYWRDAKKSAIVLS
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VPHSPQEKQEEIEALSEIIEEPQAMKEVEKPVESAPEKDNESLEAPEIINEPIRRVLV
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LTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLVLMSLTYIASWFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="C.
#06A7.3a) "
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db_xref="GI:5596653"
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cDNA EST CEMSF72FB comes from this
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                                                                215278 bp
rp23-317e13 n
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Pred. No. 12;
0; Mismatches
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                                                                   A linear ROD 18-SEP-2003
strain C57BL/6J, complete
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SOURCE
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Direct Submission
Submitted (24-UMP-2003) Department of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
6 (Dases 1 to 215278)
Song,L., Jiang,X., Swank,R. and Roe,B.A.
Submission
Submitted (18-SEP-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (20-JUN-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Direct Submission
Submitted (11-UN-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (03-UUR-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Song, L., Jiang, X., Swank, R. and Roe, B.A.
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The University Of Oklahoma
Center code:UOKNOR
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On Sep 18, 2003 this sequence version replaced gi:32171311.
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5 (bases 1 to 215278)
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SUMMARIES

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D Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss. 11-FEB-1997; WO9730160-A1. DNA encoding LA11.1 esterase es2. 27-AUG-2003 16-FEB-1998 AAT79331; AAT79331 standard; DNA; 605 BP. 21-AUG-1997 Unidentified. (revised) (first entry) 97WO-US002039.

16-FEB-1996; 96US-00602359.

(RECO-) RECOMBINANT BIOCATALYSIS INC.

Robertson DE, Murphy D Warren PV, Kosmotka A, Murphy D, Reid J, Callen W; Maffia AM, Link S, Swanson

RV;

WPI; 1997-425035/39. P-PSDB; AAW23078.

Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese or paper manufacture, and to study plant resistance to disease.

Disclosure; Page 63-64; 113pp; English.

This DNA sequence codes for LA11.1 esterase es2 (AAW23078). Newly identified polynucleotides (AAW79321-40) encoding esterases (AAW23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method

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                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                           Rice gene, SEQ ID 5263.
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                                                                                                                                                                                                                                                                                                  infection; fungal infection; viral infection;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 5263; 899pp; English
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39; Conserv
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                                                                                                                                                                    AAWWAAKTKOKIMGWIGAKTRGRARKARYWWKWATWCATKRWWIKGKGAKWAWTWMAKAWR
                                                                                                                                                                                                                                                                                                                                          GATCAAACGTTATCTAGAATCGCGCGCACCGTCCTGTGAAACCCCTCTCCCATGTCGTCGC
                                                                                                                                                                                                                                                                                                                                                                                SRMSRWKSTICYWRKWGSMKSTICTWMYYMSKYTYAKYGSYWRYRYRAWCWYMWRWYYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAMACCATTAGCTACAACTCACTCGCTATCGATGATGAGGCCATTTTTCGCCGGCCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
GACAGATCATATCGCGATATCCAC 533
                               WYWYCTTWKMACGRATKYMCCAGWWAMYSYSWTRTYWMRTWRWWWASSRTAKRMARMWWK
                                                            GCGCGATCCACTGGACTCCGATGGTACCGTCACAGTAGAAGAAACCAAAATAGCTGGCAT 509
                                                                                                 KYYMSWMRAWYYYXKTRRIRYKTCWWKARWGSWAYWRWWKGSAKMWWWWKGGRWGWTKY
                                                                                                                                  TCCACAAAAATCAGGCAGTATTGCAGGAACGATACCTTTAGGGCTGCGCAGCCTTTTACT
                                                                                                                                                                                                     GGTGGCACTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGAATCCCGCTA
                                                                                                                                                                                                                                      RYATRMMMMYRYSMKWYTWCTMWGYWWYWWRTYMKORYMWYKCTKTYWYWSATYWTGTW
                                                                                                                                                                                                                                                                         CATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATTGAGCAATTAGGTTTAGG
                                                                                                                                                                                                                                                                                                            RSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWKMWR
                                                                                                                                                                                                                                                                                                                                                                                                                  CCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCGGACACAGTTTGGGCGGATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMSYYASCMKSARKAGAKMCKRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMRYCARKKYSYSAARKARCWYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCSWYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 37.2; DB 7; ilarity 7.7%; Pred. No. 0.11; Conservative 231; Mismatches 234;
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.2; D:
Pred. No. 0.11;
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e Z, Zhu
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RESULT 3
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                                                                                                                                                                                                                                                       The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CP bisulphite, of genes associated with tumour suppression and oncogenes CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and CC 500 are missing from the sequence listing) sequences (Ss) and sequences CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid. CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of CC probes for detecting the cycosine methylation state and/or single CC nucleotide polymorphisms and also be used in an array for analysing CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or CC epigenetic parameters for the diagnosis and/or therapy of existing CC diseases or the predisposition to specific diseases, by analysing CC cytosine methylations. The parameters may be compared to another set of CC genetic and/or epigenetic parameters, the differences serving as basis CC for diagnosis and/or prognosis events which are disadvantageous to CC data for this patent did not form part of the 533 genomic sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at
                                                                                                                                                       Matches
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                              Sequence 26997 BP; 7233 A; 354 C; 6190 G; 13220 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzi diseases associated with cytosine methylation state e.g. cancer.
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06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UTN-2000; 2000DE-01032559.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressor gene derived chemically modified sequence
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPIGENOMICS
  CTACAACATTTATCAACTTCGACACTAATACCACTCGAAACCAAATCACTCTTTAAACAA
                                                                         TCTCCATCGAAACTAACACAATCCATAATACAAATTAAACACTAAATACACGTTAATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 471; 27pp; English.
                                    CTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGAATCCCGCTATCCACAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                TCACCTTTGCAAGGAGCTTCCATTGTCAATAAATTGAGCAATTAGGTTTAGGGGTGGCA
                                                                                                                                                     Conservative
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                                                                                                                                                                     6.6%;
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                                                                                                                                                     Score 36.8; DB 4;
Pred. No. 0.57;
0; Mismatches 127;
                                                                                                                                                                                         Length 26997;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel reagent for diagnosis, molecular conditions and therapy of chronic inflammatory joint diseases, and other inflammatory disorders, infective or tumour diseases in humans. The products of the invention have antiinflammatory, cytostatic, antirheumatic and immunosuppressive activity and can be used for gene therapy. The reagent of the invention and any proteins and can be used for medical diagnosis; (ii) for diagnosis and characterisation of chronic joint diseases, on the basis of molecular characterisation, and chronic joint diseases, on the basis of molecular characterisation, and cetermining the etiological pathogenicity principle of as yet uncharacterised inflammatory diseases, also monitoring progression and/or treatment of disease, and optimisation of therapy and (iii) for diseases, and optimisation of therapy and (iii) for continuous of disease, and optimisation of therapy and continuous. ACA64801-ACA64965 represent human polynucleotides used in the method of the invention
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                 Sequence 115218 BP; 35618 A; 23477 C; 22286 G; 33837 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
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                                                                                                                                                                                                                                                       52.7%;
                                                                                                                                                                                                                            Score 35.6; DB Pred. No. 3.1; 0; Mismatches
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The sequence is that of an ambiguity-maximised human telomerase protein coding sequence. The sequence, or specific fragments of it, can be used to modulate expression of a telomerase transcript (by hybridising to it intracellularly), e.g. for treatment or prevention of cancer, restenosis, conflammation, myocardial infarction, glomerulonephritis, transplant cripetion and infections (e.g. with human immunodeficiency virus). It can be used to express recombinant telomerase protein which can be used to be used to express recombinant telomerase protein which can be used to telomerase to its binding target. Those that inhibit telomerase activity can be used to treat the conditions listed above, while those that are caponists can be used to extend the life of proliferation-restricted caponists can be used to extend the life of proliferation-restricted calls, especially normal somatic cells, e.g. in cases of hypersensitivity or atrophy, also to improve production of recombinant proteins by calling used for bone marrow transplants. They may also be used for bone marrow transplants. They may also be used for diagnosis, Other uses of telomerase proteins are isolation, enrichment capacity, as reagent where nascent oligonucleotides of known structure are regulating cell growth/density tolerance. The agents and the telomerase considerations should be very specific, e.g. they are selective for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  telomerase; p105; treatment; prevention; cancer; restenosis; inflammation; myocardial infarction; glomerulonephritis; transplant; rejection; infection; HIV; human immunodeficiency virus; bone marrow transplants; proliferation-restricted cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV13834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding human telomerase protein p105 or its i - used for therapeutic modulation of telomerase activity and for screening for potential modulators of telomerase-target binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-101044/09.
P-PSDB; AAW41927.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 20-21; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGGTAAAGAAGAGTTGGTGAGCCT 53654
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/product= "telomerase
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This polynucleotide comprises a synthetic, ambiguity-maximised DNA coding for the p105 subunit (see AAW46593) of human telomerase. It is based on an isolated cDNA clone (see AAV05369) for p105 and encompasses all possible nucleic acids encoding the full-length protein. The invention provides methods relating to human telomerase and related nucleic acids, including the subunit proteins p140, p105, p48 and p43. The proteins may be produced recombinantly from transformed host cells or purified from human cells. Also included are human telomerase RNA (see AAV05373) and functional derivatives (see AAV05374 and AAV16092-93), as well as p105 synthetic DNA sequences (AAV05370-72). The invention also provides isolated telomerase hybridisation probes and primers capable of specifically hybridising with the telomerase gene, telomerase specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2277
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34.5%; Pred. No. 1.
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Matches 51
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2277
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                                                                                                                                                                                                                                                                                                                     Identifying at least pathogenic infection bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
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                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 5263; 899pp; English.
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F, Quan
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S, Tao
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                                                                                                                                                                                                                                                                                                                     one gene involved in plant resistance or response
for conferring resistance or tolerance to a plant
viral infection by determining or detecting plant
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Pred. No. 1.1;
25; Mismatches
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                                                                                       21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                              Wang
Wall
                                                                                                                                                                  03-OCT-2002
                                                                                                                                                                                    WO200277183-A2.
                                                                                                                                                                                                     Clostridium acetobutylicum
                                                                                                                                                                                                                                                  Prokaryotic
                                                                                                                                                                                                                                                                    19-JUN-2003
                                                                                                                                                                                                                                                                                                         ACA27498
                  P-PSDB;
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                                                                                                                                                                                                                               Antisense; ds; prokaryotic
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                                                                       ELITRA PHARM
                   ABU23628.
                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           MSWYGKSYKKKYCTWWCYMKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGTCATCGTCTGCA
                                              Zamudio
Trawick
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                                                                                                                                                                                                                                                                                                                                                                       CGACGACGAATCCCGCTATC 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTTTGGGCGGATTGGTGATCAAACGTTATCTAGAATCGCGCGCACCGTCCTGTGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTTTTCGCCGCCTTGACCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCGGACA
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                                                                                                                                                                                                                                                 essential gene
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2002US-0362699P
                                                                                                          2001US-00948993.
2001US-0342923P.
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                                                                                                                                               2002WO-US009107
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Carr (
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                                             Haselbeck R, Yamamoto R,
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                                                                                                                                                                                                                                gene; cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                              Ohlsen
Forsyth
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                                               Zyskind
Xu HH;
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(first entry)

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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) an bost cell containing the vector; (3) an isolated CC encoding a polypeptide whose expression is inhibited by the antisense CC entisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation of the test compound that influences the activity of CC identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies CC oraginism acts; (9) manufacturing an antibiots proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC which each of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the extent CC which each of the strains is present in a culture or collection of CC strains; or of or screening homologous nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, CC identifying cessential genes. Note: The sequence data for this patent did celectronic format directly from WIPO at CC for provider acids are useful cellular proliferation in cells other than S. aureus, S. typhimurium, CC in the proliferation of the printed specification, but was obtained in
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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    549
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Trawick JD,
    ₽₽;
    198
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Carr GJ,
Þ
    64 C;
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    116 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĄŞ,
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Xu HH;
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Best Local Similarity Matches 47; Conserv

5.8%; ilarity 65.3%; Conservative

; Score 32; DB; ; Pred. No. 3.7; 0; Mismatches

DB 7; Length 549;

25; Indels

0 Gaps

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RESULT 12
AH31609
ID AH311
XX AH31
XX AH31
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XX AH31
XX AH31
XX Human
XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ϋ́S
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining the interaction pattern of a difference in the olfactory, and can be used for determining
                                                                                                                                                                                                                                                                                               Sequence 936 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides which encode polypeptides involved in olf sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1999; 99US-0158615P
24-FEB-2000; 2000US-0184809P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2000; 2000WO-US027582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scent profile; scent fingerprint; scent representation; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human olfactory receptor polynucleotide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES &
            319 TTAGGTTTAGGGGTGGCACT 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                          CATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATTGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 248; 1857pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCACTAGGTAATTCAGCAGAATTTTGGGTTAAAAGAACACGACGACGACGAATCCCGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAAACAATCCG
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                                                                   CGTTTCATTGCCATCCGCAATCCTTTGAGATATGCTTCCATTTTCACCAATACTAGAGTC
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; OR; primary scent determination; determination, polypeptide library; odour r
                                                                                                                                                                                                                                                                                               214 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           & DEV
                                                                                                                                                                                                                                                                                                                                                         olfactory faculties of different individuals
                                                                                                                                                                                                            5.8%;
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                                                                                                                                                                                                                                                                                                  232 C; 174 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                 0;
                                                                                                                                                                                                            Score 32;
Pred. No.
                                                                                                                                                                                 red. No. 4.8;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glusman G,
                                                                                                                                                                                                                                                                                                  316 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        4.
                                                                                                                                                                                    30;
                                                                                                                                                                                                                                        Length 936
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                                                                                                                                                                                       Indels
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                                                                                                                                                                                    Gaps
                                                                                                                                   318
                                                                         417
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RESULT 13
ACF73424/c
ID ACF734
XX ACF734
XX ACF734
XX ACF734
XX ANTIDA
DT 20-NOV
XX ANTIDA
XX ANTIDA
XX HOZOO;
XX HOZOO;
XX HOZOO;
XX WP1;
XX 27-MAI
XX 27-MAI
XX WP1;
XX PP PSD
XX WP1;
DR P-PSD
XX New S
PT PR P-PSD
XX New S
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CC Usefi
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                                                                                                         RESULT 14
ABK65284
 BXBXBXB
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                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a partient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused \delta, aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2002; 2002WO-IB002637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID NO 2207; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001; 2001GB-00007661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
Arabidopsis cDNA encoding a transcription
                               02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                         Sequence 528 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masignani V, Mora M,
                                                                                          ABK65284 standard; cDNA; 969 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-120786/11.
                                                                                                                                                                      420
                                                                                                                                                                                                                                  62 ATCGTCTGCATAAATTGGGTTATCGTACTCA 92
                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                      and as a car
el S. aureus
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                                                                                                                                                                                                                                                             ATCTTCTGGATCATTTAGTTCTTCTTGATCA 390
                                                                                                                                                                                                                                                                                              Conservative
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                       212 A; 57
                                                                                                                                                                                                                                                                                                            59.3%;
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                                                                                                                                                                                                                                                                                                                                                                                      genes of the invention
                                                                                                                                                                                                                                                                                                                                                       C; 116 G; 143 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                            Score 31.8;
Pred. No. 4.
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                           DB 7;
   factor #136
                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                           Length 528;
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                            Gaps
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The invention relates to 1 of 33 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered cexhibits ectopic expression or altered expression of one or more genes can associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer creadable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant encombinant polynucleotide is used for producing a plant having a computed or recombinant polynucleotide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, inserting the computation, and selecting the vector into a plant or a cell of a plant to overexpress the polynucleotide or antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, inserting the compise of a selecting a polynucleotide that the polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, interest production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease environmental stress response (e.g. drought), microbial disease condition and flower sensecuce is one of the 232 polynucleotides encoding an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilgrim
Adam L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 558-559; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2000; 2000US-0227439P.
16-NOV-2000; 2000US-00713994.
18-APR-2001; 2001US-00837944.
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(DUBE/)
(HEAR/)
(JIAN/)
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(REUB/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KEDD/)
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JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RATCLIFF O. REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREELMAN R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU93098
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PINEDA
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                            transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pineda C
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Query Match

Sequence

969 BP;

267 A; 247 C; 212 G; 243

T; 0 U; 0 Other;

Score

31.8;

DB 6

149 ACCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCGGACACAGTTTGGGCGG 203	Ś
392 CTCAAACCACCAACAACTCCCTTGTTCTCCCCTGGAAAGCACGGTCGTCCACGCACAA 451	B
89 CTCAAACCATTAGCTACAACTCACTCGCTATCGATGATGAGGCCATTTTTCGCCGCCTTG 148	Ś
Query Match 5.7%; Score 31.8; DB 6; Length 969; Best Local Similarity 54.8%; Pred. No. 5.8; Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	3 m V
Sequence 969 BP; 267 A; 247 C; 212 G; 243 T; 0 U; 0 Other;	SO
information supplied to Derwent by the European Patent Office	\$88
in methods of the invention. Note: The sequence data for this patent is	38
an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) us	88
production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that	3 8
characteristic of a stress response. The method is useful in the	88
array or probes representative of the plant cell genome; and (b) derecting a profile of expressed polymiclectides in the plant cell	388
The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid	888
Claim 144; SEQ ID NO 1790; 577pp + Sequence Listing; English.	X X
Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.	K K K
I; 2002-304127/34.	双兒
Harper JF, Kreps J, Wang X, Zhu T;	Z Z
(SCRI) SCRIPPS RES INST. (SYGN) SYNGENTA PARTICIPATIONS AG.	XPA
24-AUG-2000; 2000US-0227866P. 26-JAN-2001; 2001US-0264647P. 22-JUN-2001; 2001US-0300111P.	K K K X
24-AUG-2001; 2001WO-US026685.	¥ \$
28-FEB-2002.	i g x
WO200216655-A2.	\$ B.
Arabidopsis thaliana.	\$ 23 \$
Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	₹₹\$
Arabidopsis thaliana stress regulated gene SEQ ID NO 1790.	(8)
21-JAN-2003 (first entry)	{
ABZ13985;	18 3
RESULT 15 ABZ13985 ID ABZ13985 standard; DNA; 969 BP. XX	RES ABZ
452 AACGCCCTCGTCCACCTGTCCAGGATAAAGATAGAGTCAAAGACAATGTGTGCGG 506	망
149 ACCGATCGCTCACTCATGCCTCATGCCTTAATGCTTTAGTCGGACACACAGTTTGGGCGG 203	8
392 CTCAAACCACCAACAACCTCCCTTGTTCTCCCTGGAAAGCACGGTCGTCCACGCACAA 451	Вb
89 CTCAAACCATTAGCTACAACTCACTCGCTATCGATGATGAGGCCATTTTTCGCCGCCTTG 148	ફ
HeBC LOCAL SIMILATICY 54.8%; FIEC. NO. 5.8; Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	30

452 AACGCCCTCGTCCACCTGTCCAGGATAAAGATAGAGTCAAAGACAATGTGTGCGG 506

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Search completed: April 30, 2004, 11:04:24 Job time: 233.167 secs

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10519.601 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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a; Chromadorea; chidae; Ostertag Whitton,C., Dau ell,B. Centre Nematode Centre Nematode ings, West Mains	LLIGNMENTS 526 bp mRNA 60stertagia oster d 03E06 5' simila id 03E06 5' simila	AI209943 AI209943 BY502873 AQ110347 CC1172630 CG684361 BH715417 BH533401 CNS026EJ CNS02FPO CP665213	AW342644 BQ262340 BG302675 BG302675 BI552284 BX376686 BI757625 AJ210254 AW116871 BM332415 BM332415 CA809398 CCNS037RT	BG497402 AQ451880 BX381961 CG098039 CC7711514 CA808007 BQ494475 BQ499441 BQ499441 CR608080 BX311247 CCF488002 CCN5010B7 CCCS4553 BX514834 BX554834
Rhabditida; Strongylida; giinae; Ostertagia. ub,J., Guiliano,D., e EST Project iology s Road, Edinburgh, EH9	linear EST 05-JUN-2001 tagi adults Ostertagia r to pir T16428 a chain F52E4.1, mRNA	AI209463 alb04f2.f AI20943 f0h12al.f BY582873 BY582873 BY582873 BY582873 AQ110347 CIT-HSP-2 CC172630 ZMMBBC029 CG664361 ZMMBBC015 BH715417 BOHWS93TF BH533401 BOGQN45TF AL183268 Tetraodon AL070328 Drosophil BQ107442 NXLV097 B CF665213 RTCNT1_14	AW342644 filliof.x BQ262340 fz85a08.x BQ36275 fil6b04.x BG302675 fil6b04.x BG302675 fil6b04.x BG302686 BX376686 BI757625 603027909 AI210254 h1e05al.f AW116871 fil0h05.x BM312415 MEST168-F BM312415 MEST168-F CA809398 CA1211041 CA809398 CA1211041 CA809398 Tetraoden	BG497402 602538689 AQ451880 HS 5.184 B BX381961 BX381961 CG098039 PUPNY34TD CC7115154 OGVERA5TC CC8080007 CA12LIIO4 BQ4944475 EST03541 BQ49345 EST03566 BQ49441 EST08666 BQ49941 EST08666 BQ49941 BY108666

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BG776621/c
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Plate: 03 row: E column: 06
Seq primer: LambdaGTIIPOR
High quality sequence stop: 43
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Vercruysse, Ghent University, Belgium. Sequencing was peri
Claire Whitton ICAPB, University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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BG776621.1 GI:14046938
EST.
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Tissue Procurement: ATCC
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602663771F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4809040
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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quality sequence stop: 583.
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/clone lib="0stertagia ostertagi adults"
/clone Prostertagia ostertagia constructed (5'end); Site_2:
/note="Vector: Lambda gtll; Site_1: EcoRI (5'end); Site_2:
NotI (3'end); Ostertagia ostertagi is a parasite of
cattle. The library was constructed from mENA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ostertagia ostertagi adults and produced with random hexamer primers."
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/mol_type="mRNA"
/db_xref="taxon:6317"
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="MAGE:4809040"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
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/sex="mixed"
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3:4809040 5',
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CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM874 row: 1 column: 12
High quality sequence stop: 658.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcggcctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloming as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGAGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
/mdl_type="mRNA" | foliar | fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 TCTTATCAAGATAAAATACTATTTCATGGGAAAAGCCTTTGGTCCTACTGAAATCCCCTTC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 715)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG493794
BG493794.1 GI:13455308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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ilarity 52.7%;
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/tissue_type="mucoepidermoid carcinoma"
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5'-ATTCTAGAGGCCGAGGCGGGCGACATG-dT(30) EN-3' (where B = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG497402
816 bp mRNA linear EST 27-MAR-2001
602538689F1 NTH_MGC_59 Homo sapiens cDNA clone IMAGE:4659742 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL
http://xmage.lnnl.gov
Plate: LLCM1456 row: a column: 23
High quality sequence stop: 715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 816)
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BG497402.1 GI:13458919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGTAAAGAAGAGTTGGTGAGCCT 301
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ilarity 52.7%;
Conservative
                 /clone lib="NIH_MGC 59"
/clone lib="NIH_MGC 59"
/note="Torgan: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCGGCCGACATG-dT(3)1BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Library."
                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4659742"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.6; DB
Pred. No. 6.7;
0; Mismatches
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RESULT 6
AQ451880
LOCUS
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AUTHORS
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                                                         Query Match
Best Local S
Matches 61
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MEDLINE
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                        11
                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
plate: 760 row: B column: 9
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 498)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ451880 498 bp DNA linear GSS 21-APR-1999
HS_5184_B1_A05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=760 Col=9 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Washington
401 Queen Anne Avenue North, Seattle,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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AQ451880.1 GI:4593050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the human BAC library RPCI-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                          Similarity
TTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGTCATCGTCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    act: Mahairas GG, Wallace JC,
Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 498.
Location/Qualifiers
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jwallace@u.washington.edu
                                                                                                                                          /clone lib="RPCI-11 Human Male BAC Library"
/notee="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/notee="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/notee="Vector as isolated from one randomly chosen donor
and partially disested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="plate=760 Col=9 Row=B"
                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                    sex="male"
                                                                          6.3%;
58.7%;
                                                         0
                                                         Score 35.2; DI
Pred. No. 7.6;
O; Mismatches
                                                                                          43;
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KEYWORDS
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Best Local S
Matches 23
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com l
http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO72CC03NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1201)
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BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                CTCTCCCATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATT
NYMIKKYWYMCKKBMMCKIQYKYMYNKWYVKKKKAMMIBKCVMKWKWKWKOCKKVWMBKWCAKKK
                                                   GAGCAATTAGGGTTAGGGGGCACTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACAC
                                                                                                                                                                                                                             MCCKMCCMCKKKKKMBKGKMVCMCKMMKNIKKCMCMKBMMCKMCMKMCMBKKNIMMMM
                                                                                                                                                                                                                                                                                 AGTTTGGGCGGATTGGTGATCAAACGTTATCTAGAATCGCGCGCACCGTCCTGTGAAACC
                                                                                                                                                                                                                                                                                                                                          NNINNIMMINICNENKKKANKTIMMINIMMININNIKKANIMINIKANIMINIMINIKKMKMSKEKKK
                                                                                                                                                                                                                                                                                                                                                                                                 ATTTTCGCCGCCTTGACCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCGGACAC
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                                                                                                             MEGNEGATARENKAMAKKUNTATATATAKKAMACAMACKAMAKKANAMBKKOLOMAKKAMACAMAKKKHIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 35.2; DB 13; llarity 4.9%; Pred. No. 11; Conservative 184; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) /note="lst strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="CSODIO72YF05"
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Catarrhini; Hominidae
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CC711514
CC711514.1 GI:3
GSS.
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Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 942)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:4577"
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_XB Zea mayв genomic clone ZMMBMa0501G18
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Query Match
Best Local Similarity
Transcriptional responses of Vitis vinifera bacterial pathogen Xylella fastidiosa Unpublished (2003) Contact: Doug Cook CAES Genome Facility
                                                                                                                                                                    Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
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CA12LIIO4IIF H11 Cabernet Sauvignon Leaf - CA
cDNA clone CA12LIIO4IIF_H11 5', mRNA sequence
CA808007
                                                                                                            Goes da Silva, F., Lim, H., Walker, M.A. and Cook, D.R.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 931)

whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
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Fax: 301-838-0208
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Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: whitelaw@tigr.org
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/mol_type="genomic DI
/strain="B73"
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/clone=lib="ZM 0.7_1.5_KB"
/note="Vector; pBCSK-; Site 1: HincII; 0.
methylation filtered genomic DNA library"
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0; Mismatches
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Tel: 530 754 6561
Fax: 530 754 6617
                                                                                                                                                                                                                                        Paracoccidioides brasiliensis

Paracoccidioides brasiliensis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (bases 1 to 434)

Goldman, G.H., dos Reis Marques, E., Duarte Ribeiro, D.C., de Souza Bernardes, L.A., Quiapin, A.C., Vitorelli, P.M., Savoldi, M., Bernardes, L.A., de Oliveira, R.C., Nunes, L.R., Travassos, L.R., Puccia, R., Batista, W.L., Ferreira, L.E., Moreira, J.C., Bogossian, A.P., Tekaia, F., Nobrega, M.P., Nobrega, F.G. and Goldman, M.H.
Eukaryot. Cell 2 (1), 34-48 (2003)
Contact: Gustavo Henrique Goldman
Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao
                                                                                                                                                               Expressed sequence tag analysis of the human pathogen Paracoccidioides brasiliensis yeast phase: identification of putative homologues of Candida albicans virulence and pathogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ494475
434 bp mRNA linear
EST03641 Pb0001 Paracoccidioides brasiliensis cDNA,
BQ494475
BQ494475.1 GI:24443116
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1 Shields Ave., DAvis, CA 95616, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Cabbrnet Sauvignon Leaf - CA12LI"
/clone_Togan: Leaf; Vector: pDNR; Site_1: Sfit; Site_2:
Sfit; CA12LI is a cDNA library of Cabbrnet Sauvignon_
leaves. The leaves were collected on September 20, 2001,
in Napa Valley, California, and represent leaves in late
season development. These leaves were symptomatic and
verified to be infected with the bacterial pathogen,
Xylella fastidiosa, based on a diagnostic assay using PCR
and Xylella-specific primer pairs. cDNAs were made by
oligo-off priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-ANACAGTGGTATCAACGCAGAGTGGCCATTACGGCCGG-3' and
5'-ANACCAGTGGCTATCAACGCAGAGTGGCCATTACGGCCGG-3'. Library was
constructed using the Clontech Creator SWART kit and
size-selected to contain the 0.5-3 kb size fraction."
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/sex="hermaphrodite"
/dev stage="Late season sample"
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(mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                       Eukaryot. Cell 2 (1), 34-48 (2003)
Contact: Gustavo Henrique Goldman
Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao
Email: ggoldman@usp.br.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes; Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (bases 1 to 443)
Goldman,G.H., dos Reis Marques,E., Duarte Ribeiro,D.C., de Sou Bernardes,L.A., Quispin,A.C., Vitorelli,P.M., Savoldi,M., Semighini,C.P., de Oliveira,R.C., Nunes,L.R., Travassos,L.R., Puccia,R., Batista, W.L., Ferreira,L.E., Moreira,J.C., Bogossian,A.P., Tekaia,F., Nobrega,M.P., Nobrega,F.G. and
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EST02518 Pb0001 Paracoc
BQ493352
BQ493352.1 GI:24440281
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                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tag analysis of the human pathogen Paracoccidioides brasiliensis yeast phase: identification of putative homologues of Candida albicans virulence and pathogenicity
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                          AGAAACCAAAATAGCTGGCATGACAGATCATATCGCGATATCCACCACTTCATACGAGAA 548
                                                                                          AGGGCTGCGCAGCCTTTTACTGCGCGATCCACTGGACTCCGATGGTACCGTCACAGTAGA 488
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/mol type="mRNA"
/db xref="taxon:121759"
/clone_lib="pb0001"
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/mol_type="mRNA"
/db xref="taxon:121759"
/clone_lib="Pb0001"
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Pred. No. 20;
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MY-15-C-12 PinfestansMY
BE776398
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Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - PCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag analysis of the human pathogen Paracoccidioides brasiliensis yeast phase: identification of putative homologues of Candida albicans virulence and pathogenicity
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Onygenales; mitosporic Onygenales;
(bases 1 to 485)
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EST08666 Pb0001 Paracoccidioides
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BQ499441.1 GI:24452737
 Kamoun, S., Hraber, P.T. Initial assessment of
                                                                             Phytophthora infestans (potato late blight agent)
Phytophthora infestans
                                             Phytophthora.
                                                             Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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               (bases 1 to 593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/db_xref="taxon:121759"
/clone_lib="pb0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Paracoccidioides"
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Pred. No. 21;
0; Mismatches
gene diversity for the compacte pathog
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Phytophthora infestans cDNA,
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Campus de beaulieu, F
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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98
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Onco
1 (bases 1 to 624)
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BX311247 AGENAE Rainbow trout multi-tissues subtracted library (tcay) Oncorhynchus mykiss cDNA clone tcay0023b.h.08 3prim, mRNA
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                                                                                                                    Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29591892
Contact: Guiguen Y
                                                                                                                                                                                 Govoroun, M., Guiguen, Y. and Le Gac, F. Construction and primary characteriza libraries in rainbow trout, Oncorhync
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Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and re
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/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; Total
/Note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
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/mol_type="mRNA"
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ne_lib="PinfestansMY"
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/dev_stage="from embryos to adults"
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5: /cgn2_6/ptcdata/2/ina/backfiles1.seq:*
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Sequence 203, App
Sequence 2564, App
Sequence 162, App
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US-08-232-463-14 Query Match

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APPLICATION NUMBER: EP 91 1 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: SEQUENCE GHARACTERISTICS: SEQUENCE GHARACTERISTICS: SEQUENCE HARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE TO SOURCE: SEQUENCE TO SOURCE: TYPE: Innear IMMEDIATE SOURCE: CLONE: DTZGPC-F1s	APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBI NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardne: STREET: 1800 Diagonal Road CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IN PC comparib OPERATING SYSTEM: PC-DOS/I SOFTWARE: Patentin Release CURRENT APPLICATION DATA: APPLICATION UMMBER: US/08, FILING DATE: CLASSIFICATION DATA: APPLICATION UMMBER: US/07, FILING DATE: CLASSIFICATION UMMBER: US/07, FILING DATE: CLASSIFICATION UMMBER: US/07,	28.6 -463-14 e 14, A NO. 567 L INFOR ICANT:		0000 0000 0000 40000 4000
TITON NUMBER: DATE: 26-AV BAST INFORM BENT, Stephe: AATION NUMBER ICE, DOCKET NUM NICATION INF NNE: (703) 83:-	PANT: FALKNER, F. G. OF INVENTION: RECOMBING OF SEQUENCES: 52 SPONDENCE ADDRESS: SUBSEE: FOLEY & Lardner SET: 1800 Diagonal Road f: Alexandria TE: VA TTRY: USA TTRY: USA FER READABLE FORM: FER READABLE FORM: FER READABLE FORM: TYPE: FLOPPY disk UTTYPE: TIM PC COMPACIBLE TOWN FOLOS/M WATING SYSTEM: PC-DOS/M WATING SYSTEM: PC-DOS/M WATING SYSTEM: PC-DOS/M WATION SYSTEM: PC-DOS/M WATE: PATENTION DATA: JICATION NUMBER: US/08/ APPLICATION DATA: JICATION NUMBER: US/07/ JICATION NUMBER: U	¶ 27 · · · CF	, , , , , , , , , , , , , , , , , , ,	ังเงินเนินเ
NUMBER: EP 91 26-AUG-1991 INFORMATION: Stephen A. NUMBER: 29,7 INFORMATIC (TO3) 836-9300 03) 683-4109 49 10 NO: 14 SEQ ID NO: 16 SEQ ID NO: 17 SEQ ID NO: 17 SEQ ID NO: 18 SEQ ID NO: 19	R, F. G S: RECS S: S2 RESS: Y & Lar y & Lar y & Lar y compa grown a gr	93303 4 08-09 AL ion US/08232463 . F. TINGER, F.	936 936 939 939 2063 4100 2103 2103 2103 2103 2103 2103 2103 2	
8 14 00 01 14 15 15 15 15 15 15 15 15 15 15 15 15 15	G. COMBINA COMBINA Road,	# 08 2 _		
114 300.6 68 30472/114 IMMU N:	INT: FALKNER, F. G. PINVENTION: RECOMBINANT FOWLPOX VIRUS OF SEQUENCES: 52 CONDENCE ADDRESS: SSEE: Foley & Lardner 1 800 Diagonal Road, Suite 500 Alexandria 1 VA RY: USA 22313-0299 READABLE FORY: READABLE FORY: READABLE FORY: READABLE FORY: REPORTING PC-DOS/MS-DOS MTYPE: Floppy disk TIRIC PATENTION DATA: CATION NUMBER: US/08/232,463 IFICATION NUMBER: US/07/935,313 IG DATE: PCATION NUMBER: US/07/935,313	US-09-497-855A-44 ALIGNMENTS 32463	US-08-910-501-3 US-09-398-550-3 US-08-910-501-1 US-09-398-550-1 US-09-753-655-1153 US-09-753-655-307 US-08-162-809-1 US-08-162-809-1 US-09-976-994-1039	US-09-489-039A-6730 US-09-134-000C-989 US-09-491-577-45 US-08-961-527-26 US-09-328-352-751 US-08-956-171E-23
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US-08-676-967-2/c
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                                Query Match
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                            Matches
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                                                                                        MOLECULE TYPE: cDNA
-08-676-967-2
                                                                                                                                                            TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUNDBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                              SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 268 Bush St. CITY: San Francisco
                                                                                                                                STRANDEDNESS:
                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200
                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACCCTCTCCCATGTCGTCGCCATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCCATTTTTCGCCGCCTTGACCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCG 187
TTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGTCATCGTCTGC 70
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                            Conservative
                                                                                                                     linear
                                                                                                                                    double
                                                                                                                                                                                                                                                                                                                      530
                                           6.2%; Score 34.4; DB 1; Length 2277; 34.5%; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KATHLEEN
                              25;
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                              Mismatches
                           72;
                              Indels
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Sequence 2, Application US/09098487 Patent No. 5917025

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RESULT 4
US-09-098-487-2/c
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; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-676-974-2
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Best Local
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APPLICANT: COLLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIF: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   ocal Similarity
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                                                                            542
                                                                                                                                                                                                                       662 TTYTTYTTNACNSWYTCYTGRYGYTINSWYTCRIGNSWYTTYTCYTCNCCDAINGCNSWN 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ATMANTIGGGTTATCGTACTCANACCATTAGCTACAACTCACTCGCTATCGATGATGAGG 130
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                                                                              CCYTTDATYTCYTTCATRITCATNCCYT 515
                                                                                                               CCATTITICGCCGCCTTGACCGATCGCT 158
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34.5%; Pred
twe 25;
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                                                                                                                                                                                                                                                                                                   Score 34.4; DB 1;
Pred. No. 0.065;
5; Mismatches 72;
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                                                                                                                                                                                                                                                                                                                                    Length 2277;
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GENERAL INFORMATION:

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US-08-956-171E-203/c
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Best Local Similarity 34.5
                                                                                                                                                                                                                                                                                Sequence 203, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
ANAMS: OBMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COLLINS, Kathleen TITLE OF INVENTION: Human Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 94104
                                                                                                          Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                    542
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STREET: 9410 Key West Avenue
CITY: Rockwille
STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                    CCYTTDATYTCYTTCATRTTCATNCCYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTYTTYNACNSWYTCYTGRTGYTINSWYTCRTGNSWYTTYTCYTCNCCDAINGCNSWN 603
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                                                                                          DDRESSEE: Human Genome Sciences,
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                                                                                                                                                                                                                        Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 34.4; DB 2; Length 2
34.5%; Pred. No. 0.065;
ative 25; Mismatches 72; Indels
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ER: UCB96-055
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2564, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION: ADDUCETTE-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

PILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRICE DATE: 30-Jun-1998
PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
PILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQ ID NO: 203:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4215 ATCTTCTGGATCATTTAGTTCTTCTTGATCA 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4715 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...2217;
SEQUENCE DESCRIPTION: SEQ ID NO: 2564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                      ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOETWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,637B

FILING DATE: 04-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BEALL APPLICANT: PICARD, France APPLICANT: OUBLLETTE, Marc Paul H.
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                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/526,840
FILLING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1115 AGCGGTTGCAGCAATTTGGTTATAGTTCTCAAAATGACTGCTATTATACA 1164
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T: 411 EAST WISCONSIN AVENUE
MILWAUKEE
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                    WISCONSIN
                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-SPECIFIC AND UNIVERSAL DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
  850586.90012
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US-08-526-8408-162
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                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 53202-4497
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWALE: Patentin Release #1.0, Vers
SOPTWALE: PATENTIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                             APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (414) 277-
TELEFAX: (414) 277-559
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OUBLLETTE APPLICANT: ROY, Paul TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
:NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1in MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 East
CITY: Milwaukee
STATE: Wisconsin
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Local Similarity 47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 AAGCGGGGCGGTAAATATGGTGTACGCAATGATATTGCGGTGGTTCGCATACCAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 ATTGAGCAATTAGGTTTAGGGGTGGCACTAGGTAATTCAGCAGAATTTGGGTTTAAAAGAA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAACCGATTGTGATGGCA 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8: QUARLES & BRADY
411 East Wisconsin Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROY, Paul H.
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E: DNA (genomic)
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                     (414)
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
177
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                                                                              850586.90012
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Pred. No. 0.64;
0; Mismatches 105;
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US-09-298-367B-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: BCM-03728
CURRENT APPLICATION NUMBER: US/09/298,367B
CURRENT FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/8 PRIOR FILING DATE: 1997-04-15 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Highlander, Sarah K.
APPLICANT: Federova, Natalie D.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5162
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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 CAAACCGATTGTGATGGCA 3521
                                GAAACCAAAATAGCTGGCA 508
                                                                      AAGCGGGGCGGGTAAATÁTGGTGTACGCAÁTGATÁTTGCGGTTGGTTCGCATÁCCAAÁTCG 3540
                                                                                                     GGGCTGCGCAGCCTTTTACTGCGCGATCCACTGGACTCCGATGGTACCGTCACAGTAGAA 489
                                                                                                                                         CGCAACAGGCAATCCATTGATTCGCGCTGCTACGCCAACATCGTGGAAAGTGTACGATAA 3600
                                                                                                                                                                            CACGACGACGAATCCCGCTATCCACAAAATCAGGCAGTATTGCAGGAACGATACCTTTA 429
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47.2%;
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Pred. No. 2;
0; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                        DB 3; Length 5162;
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                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vel
SEQ ID NO 5
LENGTH: 5262
TYPE: DNA
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SEQ ID NO 4
LENGTH: 5162
                                                     Best Local
Matches
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APPLICANT: Highlander, Sarah K.
APPLICANT: Federova, Natalie D.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA VACCINE
FILE REFERENCE: BCM-03728
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PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/298,367B CURRENT FILING DATE: 1999-04-22
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CURRENT FILING DATE: 1999-04-22
PRIOR APPLICATION UMBER: 08/834,455
PRIOR FILING DATE: 1997-04-15
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Highlander, Sarah K.
APPLICANT: Federova, Natalie
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA VACCINE
FILE REFERENCE: BCM-03728
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                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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ORGANISM: Artificial Sequence
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ilarity 47.2%;
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Pred. No.
                                                       ed. No. 2.1;
Mismatches 105;
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                                                                                      DB 3;
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US-09-298-367B-2/c
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APPLICANT: Lagace, Robert, E.
APPLICANT: Parterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
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Patent No. 6632636
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Best Local
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SEQ ID NO 2
LENGTH: 6850
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APPLICANT: Federova, Natalie D.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA VACCINE
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Pred. No.
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US-09-543-681A-2188
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SEQ ID NO 2188
                                                                                                                                                                                          Matches
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Best Local
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SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GARY BRETON
TITLE OF INVENTION: UNLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999.04-09
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                                                                                                                                                                                                                                                                                          LENGTH: 1488
TYPE: DNA
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ORGANISM: M. catarrhalis
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OTHER INFORMATION: Incyte template ID
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CGGTGGCATTAGATGAAGCGGTACAAATTGGTTTAGA 1199
                                                                                          CCATCGGCTCACCTTTGCAAGGAGCTTCCATTGTCAATAAAATTGAGCAATTAGGTTTAG 328
                                                                                                                           TGACCAAAAAAGCGATTGATTTGCTGAAAAACGAATGAAAATGGTTTCTTCTTACAAGTCG
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RESULT 15
US-09-328-352-2832/c
US-09-328-352-2832/c
; Sequence 2832, Application US/09328352
; Patent No. 6562258
; Patent No. 6562258
; PAPPLICANT: GATY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUVANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
ILENGTH: 1722
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2832
Search completed: April 30, 2004, 18:43:19 Job time : 76.2277 secs
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                                                                                              100
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                                                                                              GCTGATTTGCCA 89
                                                                                                                                                                                              CACCTAATAAGCGGTATÁCAGGATTTTCAATCCAGCGAAATAATCCATCACCCCACATCG 101
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
Published Applications NA:*

1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/prodata/2/pubpna/US108_PUBCOMB.seq:*

16: /cgn2_6/prodata/2/pubpna/US108_PUBCOMB.seq:*

17: /cgn2_6/prodata/2/pubpna/US108_PUBCOMB.seq:*

18: /cgn2_6/prodata/2/pubpna/US108_PUBCOMB.seq:*

19: /cgn2_6/prodata/2/pubpna/US108_PUBCOMB.seq:*

19: /cgn2_6/prodata/2/pubpna/US108_PUB.seq:*

19: /cgn2_6/prodata/2/pubpna/US108_PUB.seq:*

19: /cgn2_6/prodata/2/pubpna/US108_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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10195.950 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 271, App Sequence 1790, Ap	Sequence 18072, Ap	Sequence 1, Appli	Sequence 15368, A Sequence 1, Appli	Sequence 1460, Ap Sequence 2011, Ap	Sequence 1135, App	Sequence 1, Appli	Description Sequence 4, Appli	

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US-10-672-787-24 US-09-864-761-5612 US-10-027-632-152659 US-10-027-632-152659 US-10-282-122A-32888	US-09-764-869-1475 US-10-091-504-1475 US-10-297-577-1475 US-10-227-632-5858 US-10-027-632-5858 US-09-452-599-162 US-10-121-120-162 US-09-847-513A-1	US-10-424-599-50022 US-10-184-634-414 US-10-184-634-414 US-09-764-877-2234 US-10-27-632-125951 US-10-027-632-125952	US-10-225-066A-377 US-10-374-780A-2733 US-08-781-986A-203 US-10-329-624-203
Sequence 24, App.1 Sequence 5612, Ap Sequence 152659, Sequence 152659, Sequence 32888, A	1475 1585 162, 162,	50 50 50 50 50 50 50 50 50 50	Sequence 377, App Sequence 2733, Ap Sequence 203, App Sequence 203, App

ALIGNMENTS

Qу 121	Db 6:	Qy 6:	מם	γγ.	Query Match Best Local : Matches 55	; OTHER INFOR	NAME/KEY:) TYPE: UNA; ORGANISM:	; LENGTH: 555	TWARE		CURRENT F		엁	TITLE OF	, GENERAL IN	; Publication	; Sequence 4	RESULT 1 US-10-603-260-4
121 GATGATGAGGCCATTTTTCGCCGCCTTGACCGATCGCTCACTCA	61 CATOGTCTGCATAAATTGGGTTATCGTACTCAAACCCATTAGCTACAACTCACTC	61 CATCGTCTGCATAAATTGGGTTATCGTACTCAAACCATTAGCTACAAACTCACTC	1 ATGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGT	1 ATGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGT	Query Match 100.0%; Score 555; DB 16; Length 555; Best Local Similarity 100.0%; Pred. No. 1.6e-179; Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps	OTHER INVENTION: vall2 gene 0-603-260-4	NAME/KEY: CDS	ORGANISM: Vibrio metschnikovii RH530 FRAVURE:	555	3: KopatentIn 1.71	SEQ ID NOS:	FILING DATE: 2003-06-24	REFERENCE:	'ION: nucleotide	7 INVENTION: An alkaline lipase from Vibrio metschnikovii RH530	ADDITONT: Of COTOGRAPION	ion No. US20040009570A1	Sequence 4, Application US/10603260	260-4
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FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/603,260

CURRENT FILING DATE: 2003-06-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: KopatentIn 1.71

SEQ ID NO 1

LENGTH: 2578

TYPE: DNA

ORGANISM: Vibrio metschnikovii RH530

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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10603260
Publication No. US20040009570A1
GENERAL INFORMATION:
APPLICANT: CJ Corporation
TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530
TITLE OF INVENTION: nucleotide sequence encoding the same
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 555; Conserv
                                              1741
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                                               TTAGTCGGACACAGTTTGGGCGGATTGGTGATCAAACGTTATCTAGAATCGCGCGCACCG
                                                                TTAGTCGGACACAGTTTGGGCCGATTGGTGATCAAACGTTATCTAGAATCGCGCGCACCG
                                                                                              ATGCAGATTATTCTTGTTCATGGACTCTATATGCATGGCTTGGTAATGCATCCGCTTAGT 1620
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                                                                                                                                                                                                                                            100.0%; illarity 100.0%; Conservative 0;
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; Pred. No. 4e-179;
0; Mismatches 0;
                                                                                                                                                                                                                                                                    Length 2578;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENERCCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: PCTEP01/02955
PRIOR APPLICATION NUMBER: DC 10013847.0
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DC 10019173.8
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 473
LENGTH: 26997
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: REPARTION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-473
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US-10-221-714A-473/c
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                                                                                                                                                                                                                                                                                                                                               Query Match 6.6%;
Best Local Similarity 47.1%;
Matches 113; Conservative
                                                                                                                                                                                                                                                  13416 TCTCCATCGAAACTAACACAATCCATAATACAATTAAACACTAAATACACGTTAATTTC 1335
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                                                 ATARAATAAAACTACAAAAACGCTACCCTATATACTACAAAATATCCCCCGACCTCTAC 1323;
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                                                                                         AAATCAGGCAGTATTGCAGGAAACGATACCTTTAGGGCCTGCGCAGCCTTTTACTGCGCGAT
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CCACTGGACTCCGATGGTACCGTCACAGTAGAAGAAACCAAAATAGCTGGCATGACAGAT 516
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Pred. No. 1.4;
0; Mismatches 127;
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RESULT 5
US-09-783-590-1460
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, NAME/KEY: misc feature
, LOCATION: (1)...(32185)
; OTHER INFORMATION: n = A,T,C or
US-10-087-192-1135
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                                                                 PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1460
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SEQ ID NO 1135
LENGTH: 32185
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                                                                                                                                                                                             APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric
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ORGANISM: Homo sapiens
                                              ENGTH: 435
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Local Similarity 49.4%;
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Pred. No. 28;
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RESULT 6
US-10-087-192-2011/c
US-10-087-192-2011/c
; Sequence 2011, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: MOTTIS, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AN
; TITLE OF INVENTION: CANCER

FILE REFERENCE:

529452000122

AND METHODS

FOR

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NAME/KEY: misc feature
LOCATION: (414)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (335)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (379)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                         107 ACTÇACTCGÇTATCGATGATGAGGÇCATTTTTCGCCGCÇCTTGACÇGATCGCTÇAÇTÇATG 166
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                                                                                                                                                                                                                                                                        Similarity
                                                                                            CCTCGCCTAATGCTTTAGTCGGACACAGTTTGGGCGGATTGGTGATCAAACGTTATCTAG 226
                                                                                                                           GGCCTAAAACAGCTCTTTAAAAATCTATTTTTTTAGGCCAGGTGCGTTGGCTCACACCTG
                                                                                                                                                                                           TGGTTCCGCTTCAGAGCAGACTGGGNAAANTNAGGCTTACAATGGGAATNAGATGCTGTG 176
ACCAGCCTGGCCAATATGGTGGAAACCTTTACC 329
                             AATCGCGCGCACCGTCCTGTGAAACCCTCTCCC 259
                                                                                                                                                                                                                        TGCATCCGCTTAGTCATCGTCTGCATAAATTGGGTTATCGTACTCAAACCATTAGCTACA
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                       46.5%;
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Pred. No. 2.5;
0; Mismatches
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CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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Best Local S
Matches 72
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2011
LENGTH: 96499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15368, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NAME/Key: misc_feature
LOCATION: (1)...(96499)
OTHER INFORMATION: n = A,T,C or G
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                                                   FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/
FILING DATE: 2000-11-27
                                                                                                               FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                          FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
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                                                                                                                                                    APPLICATION NUMBER: 60/230,347
                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9513 TCAAACAGCCTAGCACGAATCTCTGTCTAGTTTGAAACCATACACACAGTTTTGGTTGCT 9454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 TTGACCGATCGCTCACT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 TCTATATGCATGGCTTGGTAATGCATCCGCTTAGTCATCGTCTGCATAAATTGGGTTATC
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l Similarity 52.6%;
72; Conservative
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Zyskind, Judith
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Malone, Cheryl
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NUMBER: 60/267,636
                                    NUMBER: 60/257,931
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Pred. No. 62;
0; Mismatches
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; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
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                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-10-067-514-1
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APPLICANT: Reynisdottir, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15368
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Jonsdottir, S
APPLICANT: Reynisdottir,
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                                                                   1602602
1602542 CATTGCTACTGGGGTATGGTAGCTTCTAGACCCTCTCGGCTG 1602501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 ACTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGAATCCCGCTATCCACA
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                                                                   TCTTGGTTCCTTTTACCAGAGAATGGTATTAGAAACCAAAATGAGGGTGCTAAGTGTGCT
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                                                                                                                                                                                                       5.8%; ilarity 50.0%; Conservative
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Pred. No. 4.7;
D; Mismatches 117;
                                                                                                                                                                                                       Score 32.4; DB 15;
Pred. No. 4.9e+02;
0; Mismatches 81;
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RESULT 10
US-10-087-192-226/c
US-10-087-192-226/c
; Sequence 226, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(653122
CTHER INFORMATION: n =
US-10-087-192-226
                                                                                                                                                                                                                                                 APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000112
CURRENT APPLICATION UNMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-30
PRIOR FILING DATE: 2001-03-02
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; ORGANISM: Homo sapiens
US-10-419-723-1
                                                                                                                                                         SEQ ID NO 226
LENGTH: 653122
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APPLICANT: Reynisdottir, Sigridur Th.
APPLICANT: Thorleifsson, Gudmar
APPLICANT: Gulcher, Jeffrey
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
FILE REFERENCE: 2345.2010-005
CURRENT APPLICATION NUMBER: US/10/419,723
CURRENT FILING DATE: 2003-04-18
CURRENT FILING DATE: 2003-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 10/067,514
PRIOR FILLING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 09/811,352
PRIOR FILLING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 87
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                        TYPE: DNA
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Pred. No. 4.9e+02;
0; Mismatches 81;
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                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Campylobacter jejuni
US-10-282-122A-18072
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NUMBER OF SEQ ID NOS
SOSTWARE: Patentin v
SEQ ID NO 18072
LENGTH: 549
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US-10-282-122A-18072
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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Matches
                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/230,347
392 CACAAAAATCAG 403
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                                                                                     332 TGGCACTAGGTAATTCAGCAGAATTTGGGTTAAAAGAACACGACGACGACGAATCCCGCTATC
                                                       428 TGATACTTGGAAATCCTGCAAAATTTGTGCGTGAATTAAACGATGAAGAAGTCAGCTTTC 487
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                                                                                                                         h 5.8%;
Similarity 65.3%;
47; Conservative
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Malone, Cheryl
Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                        Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                       NOS: 78614
                                                                                                                                                                                                                                                                                        version
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Pred. No. 6.3;
0; Mismatches
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Pred. No. 3.5e+02;
0; Mismatches 33;
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                                                                                                                             25;
                                                                                                                                                               Length 549;
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MB1-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT ELING DATE: 2001-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 271
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US-09-934-455-271
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%;
Best Local Similarity 54.8%;
Matches 63; Conservative
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APPLICANT:
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                                                                                                                                                                                                                                                                                                                                                                                                              CANT:
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Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
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                                                                                                                                                                                                                                                                                                                                      Riechmann, Jose Luis
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                   Reuber, Lynne
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o. US20030121070A1
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Pred. No. 10;
0; Mismatches 52;
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR REPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1790
LENGTH: 969
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(969)
OTHER INFORMATION: G1835
US-09-934-455-271
                                                                                                                 RESULT 15
US-10-225-066A-377
; Sequence 377, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
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-09-938-842A-1790
                                                         APPLICANT: Mendel APPLICANT: RATCLI APPLICANT: RIECHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                                                                                                                                                                                                                                                                                                            149 ACCGATCGCTCACTCATGCCTCGCCTAATGCTTTAGTCGGACACAGTTTGGGCGG 203
                                                                                                                                                                                                                                                                                                                                                      392 CTCAAACCACCAACAACCTCCCTTGTTCTCCCCTGGAAAGCACGGTCGTCCACGCACAA
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1 Similarity 54.8%;
63; Conservative C
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                                                     RATCLIFFE, Oliver
RIECHMANN, Jose Luis
DUBELL, Arnold T
HEARD, Jacqueline E
                                     ADAM, Luc J
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                                                                                  Biotechnology, Inc.
IFFE, Oliver
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Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.8;
Pred. No. 10;
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APPLICANT: PILGRIM, Marsha L
APPLICANT: CA1-Zhong
APPLICANT: CA1-Zhong
APPLICANT: RUBBR, T. Lynne
APPLICANT: RUBBR, T. Lynne
APPLICANT: CERLMAN, Robert A
APPLICANT: PINEDA, Omalia
APPLICANTON UNDERS: US/10/25,066A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 0/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICANTON UNDERS: 0/35,049
PRIOR APPLICANTON UNDERS: 0/35,
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90.55 90.55 90.55 90.55 90.55 90.55 90.55 90.55

AAR88011 AAR88011 AAR88011 AAR77245 AAW3393 AAW3393 AAW23073 ABU56926 ABG7597 AAR85077 AAR85077

Aae38797 Aar85077

Aar79118

Mature Ps
Mature Ps
Mature Ps
Mature Ps
P. cepaci
Pseudomon
Thermococ
Thermo

Aaw53933 Aaw23073 Abu56926 Abg75902

Aar88011 Aar77245 Aar88010 Aar88012

ALIGNMENTS

Aaw09622 Aaw61276 Aaw66101 Aab73542

Aaw09620 Aag45743 Aag45742 Aag45741 Aar34633

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Result
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This protein compolynucleotides which are claimed in host cells Torganic solvents chiral compounds industries. A meamine acid to an may also be usef	which is active in organic manufacture, and to study Disclosure; Page 63-64; 11	Robertson DE, Murp Warren PV, Kosmotk WPI; 1997-425035/39 N-PSDB; AAT79331.	11-FEB-1997; 97WO 16-FEB-1996; 96US (RECO-) RECOMBINANT	reedsturr. Unidentified. W09730160-A1. 21-AUG-1997.	LAll.1 esterase Esterase; therm paper; lignin r	AAW23078; 27-AUG-2003 (: 17-FEB-1998 (:	RESULT 1 AAW23078 ID AAW23078 standard;
This protein comprises LA11.1 esterase es2. Newly identified polynucleotides (AAT79321-40) encoding esterases (AAW23069-88), som which are claimed, can be used for recombinant production of the en in host cells. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pur chiral compounds used in pharmaceutical, agricultural and other che industries. A method is claimed for transferring an amino group from amino acid to an alpha-keto acid using a claimed esterase. The enzy may also be useful as ripening starters in cheese making, in lignin	encoding heat stable esterase from thermophilic bacteria five in organic solvents, useful in cheese or paper and to study plant resistance to disease. Page 63-64; 113pp; English.	, Murphy D, Reid J, Maffia AM, Link S, Swanson Kosmotka A, Callen W; 5035/39. 9331.	97WO-US002039. 96US-00602359. INANT BIOCATALYSIS INC.		esterase es2. e; thermostable enzyme; ester; chiral compound; cheese; pu fignin removal; sugar; lignocellulose; disease resistance;	(revised) (first entry)	ard; protein; 201 AA.

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; Pred. No. 0.05
18; Mismatches
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20-MAY-1988;
27-JUL-1988;
                                     Amino acid sequence encoding a Pseudomonas lipase. Used as a lipid-hydrolysing enzyme for oils and fats processing, in medicine, diagnosis, in detergents and digestants. It can catalyse ester hydrolysis, ester synthesis or ester conversion, in the prodn. of chemical prods. esp. optically active cpds. The DNA can be obtd. from P. fragi and cloned and expressed in E. coli. (Updated on 25-MAR-2003 to correct PR field.)
  Sequence
                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                      DNA coding
                                                                                                                                                                                                                                                                                                WPI; 1989-166833/23.
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41; Conservative
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Pred. No. 0.05
L8; Mismatches
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99US-014524P 99US-0145913P 99US-0145913P 99US-0146386P 99US-0146389P 99US-0147303P 99US-0149732P 99US-0149732P 99US-0149732P 99US-0149732P 99US-0151066P 99US-0151066P 99US-0151303P 99US-0151066P 99US-0151303P 99US-01

26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 10-AUG-1999; 11-AUG-1999; 12-AUG-1999;

27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;

10-SEP-1999; 13-SEP-1999; 15-SEP-1999;

16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 28-SEP-1999; 29-SEP-1999;

05-0CT-1999 07-0CT-1999 07-0CT-1999 13-0CT-1999 13-0CT-1999 13-0CT-1999 14-0CT-1999 14-0CT-1999

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RESULT 6
ADRA48085
AD ATA48085
AD ATA48085
AD ATA48085
AC ADRA
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Best Local Similarity
Matches 51; Conserv
                                                                                   This sequence represents the P. fragi lipase protein. This lipase has high thermostability and is active at acid pH. A varient of the mature lipase A in which phe29 has been replaced by a Trp residue has increased specific activity compared to the parent lipase. The lipase or varient may be used in ester hydrolysis, ester synthesis or interesterification. They can also be used for avoiding pitch trouble in the process for the production of mechanical pulp or a paper-making process using mechanical pulp. They can also be used in detergents or as a digestive enzyme, eg. in the treatment of cystic fibrosis. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipase A; thermostability; specific activity; mechanical pulp; ester hydrolysis; ester synthesis; interesterification; acid p
                                                                                                                                                                                                                                                                                                                                                                                                                                          New lipase variants, partic. from Candida antartica - have aminoacid substitutions to increase specific activity against substrates compared to parent lipase(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         paper-making; detergent; digestive enzyme; cystic fibrosis
   Sequence 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 41-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Svendsen A,
Hansen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1992;
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19-JUL-1994
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                                                             the treatment field.)
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RESULT 7
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Best Local S
Matches 51
                                              The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A. baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                          New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5069; 328pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     baumannii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry
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Pred. No. 0.051
31; Mismatches
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9.051;
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Query Match Best Local S Matches 39

l Similarity 39; Conserv

Conservative

10.3%; Score 96.5; 29.5%; Pred. No. 0.1 tive 18; Mismatches

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Length 453; Indels

42; 6

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                                                                                           The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are single-stranded probe comprising the nucleic acid. The nucleic acids are single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. faecium protein sequence SEQ ID 4594.
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                                                                     treating Enterococcus fone if the disclosed E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; urinary tract infection; abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 NLLEDLVQRNPRITSIDLIGHSMGGLVSRSALFYGKQNMYQWIHMVENLVCIGSPHHGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VILVHGLCMNHLTWSNAHYGGIGERLLAQRDHNIMLYLNYNIGRRISANGRS----FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IILVHGLYMH------GLVMHPLSHRLHK----LGYRT-QTISYNSLAIDDEAIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC91313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VLERFGFAL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4594; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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98US-0085598P.
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Sequence 316 AA;

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Best Local S
Matches 35
                                                                                                                                Query Match
Best Local (
                                                                                                                       Matches
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25-MAR-2003
12-FEB-1990
                                                                                                                                                                                                      The polypeptide has good stability and high lipase activity. It is use for prodm. of fatty acids from triglycerides, as a reagent for quantitative analysis of troglycerides, and as a catalyst for transesterifying fats and oils. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to standardise OS
                                                                                                                                                                                                                                                                                                               New polypeptide with lipase activity - used for prodn. from tri:glyceride(s), etc.
                                                                                                                                                                    Sequence 319 AA;
                                                                                                                                                                                                                                                                                        Claim 1; Page 12; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-293865/41.
                                                                                                                                                                                                                                                                                                                                                                                      Sagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN91331
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                (TOXN ) TOYO JOZO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
 104 IEQLGLGVALGNSABFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 LGNSAEFGLKEHDDESRYPOKSGSIAGTIPLGLRSLLLRDPLD----SDGTV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 VVS------NRY-QDYQQMIGNIPITTRFFLIAGQLDETDLSDGTV
                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVGHSLGGLVIKRYL----ESRAPSCETLSHVVAIGSPLQ---GASIVNKIEQLGLGVA
                        66 LAYVKQVLAATGATKVNLIGHSQGGLT-SRYVAAVAP--QLVASVTTIGTPHRGSEFADF
                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                              3 IILVHGL------YMHGLVMHPLSHRLHKLGYRTQTISYNSLAIDD-----EAI
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                                                                                                                                  Similarity
                                                                        VILVHGLAGTDKFANVVDYWYGIQSDLQSH-----GAKVYVANLSGFQSDDGPNGRGEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVGHSMGGVSALRYLGTYGQDTSLPQVQTLT---AIGAPFNDFVDDSAQSLTDELAKGPA
                                              FRRLDRSL--THASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNK 103
                                                                                                                                                                                                                                                                                                                                                                                        Ohta H,
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with lipase activity
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                                                                                                                                                                                                                                                                                                                                                                                         Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                  10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 96; DB 31.2%; Pred. No. 0.00 tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        ۲
                                                                                                                   33;
                                                                                                                                  Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         Imamura
                                                                                                                       Mismatches
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                                                                                                                                  DB 1;
0.081;
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•
                                                                                                                                            Length 319;
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                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                              of fatty acids
                                                                                                                       62;
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AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The sequences are based upon the wild-type P. glumae sequence disclosed in EP407225-A (UNILEVER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large
                                                         Claim 12;
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 Misc-difference
                                                                                                                                        Mutant; lipase; hydrophobicity.
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RESULT 1: AAR88009 ID AAR8

AAR88009

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                                                                                                                                                                                  Local Similarity
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                                                            104 IEQLGLGVALGNSAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTV---
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                                                                                                       FRRLDRSL--THASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNK 103
SHNTDQDALAALRTLTTAQTATY
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                                                           AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The sequences are based upon the wild-type P. glumae sequence disclosed in EP407225-A (UNILEVER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. the lipase variants show improved in-the-wash lipolytic activity and may be used in enzymatic detergent compens. (Updated on 16-OCT-2003 to standardise OS field)
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/note= "Phe to Arg, in wild-type sequence a Phe residue
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                                                                                                                                                                                                                                                                             Sequence 319 AA;
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Search completed: April 29, 2004, 11:35:16 Job time : 60 secs

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Result
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     Score
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1 MQIILVHGLYMHGL
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
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3: pir3:*
4: pir4:*
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     MQIILVHGLYMHGLVMHPLS.....KIAGMTDHIAISTTSYENAV 185
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H87675	H83755	T47566	G82119	D81675	E83729	S47087	S38635	E81578	E86533	D75007	B70906	T01149	H82134	A83712	AG2426
hydrolase, alpha/b	hypothetical prote	hypothetical prote	probable esterase/	polymorphic membra	adenine deaminase		blastopia polyprot	conserved hypothet		lysophospholipase	probable lysophosp	probable acetone-c	ъ	hypothetical prote	hypothetical prote

ALIGNMENTS

RESULT 2 \$76547 hypotherical protein - Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. A;Pariety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 C;Accession: \$76547 R;Kaneko, T; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudana Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis. A;Reference number: \$74322; MUID:97061201; PMID:8905231	1 MOIILVHGLYMHGLVMHPLSHRLHKLGYRTQTISYNSLAIDDEAIFRRLDRSLTI : :::	RESULT 1 B82501 C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82501 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: B82501 A;Carostus: preliminary A;Carostus: preliminary A;Carostus: preliminary A;Carostus: preliminary A;Carostus: preliminary A;Caross-references: GB.AE004352; GB:AE003853; NID:9952301 A;Experimental source: serogroup 01; strain N16961; biotype El Tor C;Genetics: A;Genetics: A;Genes: VCA0992 A;Map position: 2 Ouery Match Best Local Similarity 59.1%; Pred. No. 1.4e-40; Matches 104; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

GANFEKKVSAAAWE 188

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A;Cross-references: GB:AB003851; NID:g9112238; PIDN:AAF85601.1; GSPDB:GN00130; XFSC:XFad A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HBriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HBriones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiguchado, M.A.; Madeira, A.M.B.N.; Marxino, C.L.; Marques, M.V.; Martins, E.A.; Mathors: Martins, E.M.F.; Matskuma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.C.; de Rosa J.T., V.E.; de Sa., R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr.; W.A.; da Silva M.R.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2, A.Reference number: A59328
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DAA
A;Residues: 1-249 <KMN
A;Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10393.1;
A;Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; Data Library, June
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A; Note: plasmid
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A; Residues: 1-251 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: The genome sequence of the plant pathogen Xylella fastidiosa. A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: H82864
R;anonymous, The Xylella fastidiosa Consortium
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein XFa0032 [imported] - Xylella fastidiosa (str
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: XFa0032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                  IILVHGLYMHGLVMHPLSHRLHKLGYRTQTISYNSLAI--DDEAIFRRLDRSLTHASPNA
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     GMTDHIAISTTSYE
                                                                                                         FGLKEHDDESRYPQKSG-----
                                                                                                                                                                 LVGHSYGGAVI----TEAGODERVKALVYIAAFAPSEGESVA---
                                                                                                                                                                                                                   LVGHSLGGLVIKRYLESRAPSCETLSHVVAIG--SPLQGASIVNKIEQLGLGVALGNSAE 118
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                                                       -----DLNKKYPLPSGYNHLSSDKEGFLMLTPEGVEKYLAQDIPLEQTRLIIATQHPIR
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                                                                                                                                                                                                                                                                                                                                                                                    Score 112.5; DB Pred. No. 0.011; 3; Mismatches
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hypothetical protein SMa2023 [imported] - Sinorhizobium meliloti (strain 1021) (c;Species: Sinorhizobium meliloti (c;Species: Sinorhizobium meliloti (c;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 c;Accession: C95400 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Ritle: Nuclectide sequence and predicted functions of the entire Sinorhizobium A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                  A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243 < KUR>
A;Residues: 1-243 < KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65765.1; PID:g14524263; GSPDB:GN00165
A;Cross-references: GB:AE006469; PIDN:AAK65765.1; PID:g14524263; GSPDB:GN00165
A;Cross-references: GB:AE006469; PIDN:AAK65765.1; PMA
A;Experimental source: strain 1021, megaplasmid pSymA abola, P.; Ampe, F.; Barloy-Hubler
A;Galibert, F.; Finan, T.M.; Long, S.R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauxe
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauxe
A;Authors: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE008687; PIDN:AAL45901.1; PID:g17743647; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, P.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Goi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein Atu5212 [imported] - Agrobacterium tumefacies C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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AG3185
A; Contents: annotation C; Genetics:
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A;Genome: plasm:
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A; Residues: 1-229 < KUR>
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28.3%; Pred. No. 0.0
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                 lactonizing lipase VCA0221 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae (c;Decies: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82486 ___
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A;Note: the nucleotide
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A; Residues: 1-202 < KAN>
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A;Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Synechocystis sp.
A;Variety: pCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997
C;Accession: S77556
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Best Local S
Matches 39
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Similarity 24.5%;
39; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                               SPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKIEQLGLGVGALGNS 116
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Pred. No. 0.052;
29; Mismatches
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A;Accession: C82486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <HEI>
A;Cross-references: GB:AE004362; GB:AE003853; NID:g96576
A;Experimental source: serogroup O1; strain N16981; biot
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitroger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein alr1352 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AE1975
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AE1975
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A;Map position: 2
C;Superfamily: Pseudomonas triacylglycerol
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A;Accession: AE1975
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Best Local S
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                                                                                                                                                 69 PEOPFDLVGFSMCG-IVSRYYVOKLGGISRVQRFVTISSPHHGTVVAYASQHPGCVQMRP 127
                                                                                                                                                                                                                           11 VLÍVHGITDTETVFNÉMAVYLRQLGWTVYŤL--NLVPNNGEAPLNVLAQQVADYVCATIT
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                                                                                                                                                                                                                                                              3 IIIVHGLYMHGLVMHPLSHRLHKLGYRTQTISYNSLAIDDEAIFRRLDR-----SLT
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                                                                                                               NSAEFGLKEHD---
                                                                        NSLFLQDLNRDVQMLEQLNFTSIWTPYDLMIIPTHSSKMPVGKELTIPVALHSWMLKD
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                                                                                                               DESRYPOKSGSI-AG---TIPLGLRSLLLRD 152
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Bl Tor
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                                                                                                                                                                                                                                                                                                        31,
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A; Experimental source: IFO-12049
R; Kugimiya, W.; Otani, Y.; Hashimoto, Y.; Takagi, Y.
Biochem. Biophys. Res. Commun. 141, 185-190, 1966
A; Title; Molecular cloning and nucleotide sequence of the lip
A; Reference number: A26383; MUID:87100109; PMID:3800995
A; Accession: A26383
A; Molecule type: DNA
A; Residues: 1-118, 'CAWPLSRGGLAKRWLPP' < KUG>
A; Cross-references: GB:M14604; NID:g15132; PIDN:AAA25879.1;
C; Superfamily: Fseudomonas triacylglycerol lipase
C; Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                         C; Species: Pseudomonas aeruginos.
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-DC; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence; C; Accession: G83044
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
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C;Species: Pseudomonas fragi
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1000 #----
                                                                                                                                                                                            A;Cross-references: GB:AE004894; GB:AE004091; NID:g9951076; PIDN:AAG08198.1; A;Experimental source: strain PAO1 C;Genetics:
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G83044
lipase LipC PA4813 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A;Molecule type: DNA
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A;Reference number: A82950;
A;Accession: G83044
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Best Local S
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;Date: 10-Sep-199 #sequence revision
;Accession: 802005; A26383
;Aoyama, S.; Yoshida, N.; Inouye, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Pseudomonas aeruginosa
;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000;Accession: G83044
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3 IILVHGLYMHGLV-----MHPLSHRLHXLG---YRTQTISYNSLAIDDEAIFRRLDR--S | : | | | | : | : ::: : :
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                                                                                                                                                     Pseudomonas triacylglycerol lipase
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                                                                  Conservative
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                         10.3%; buc No. v. 27.7%; Pred. No. v. rive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                    sequence of Pseudomonas aeruginosa
50; MUID:20437337; PMID:10984043
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                                                                                     Score 96.5; DB
Pred. No. 0.38;
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PMID:3060375
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                                                                                                                                                                                                                                             GSPDB:GN00:
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K.; Lim,
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C;Species: Pseudomonas glumae
(;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48952; S36248; S37291
R;Frenken, L.G.; Egmond, M.R.; Batenburg, A.M.; Bos, J.W.; Visser, C.; Verrips, Appl. Environ. Microbiol. 58, 3787-3791, 1992
A;Title: Cloning of the Pseudomonas glumae lipase gene and determination of the A;Reference number: A48952; MUID:93119130; PMID:1476423
A;Accession: A48952; MUID:93119130; PMID:1476423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-327 <OLI>
A;Cross-references: EMBL:AL034492; PIDN:CAA22509.1; GSPDB:GN00070; SCOEDB:SC6C5.11
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Ollver, K.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, December 1998
A;Reference number: Z21579
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                  A;Cross-references: EMBL:X70354; NID:g49205; PIDN:CAA49812.1; PID:g49206
A;Experimental source: PG1
A;Note: sequence extracted from NCBI backbone (NCBIN:121572, NCBIP:121573)
R;Frenken, L.G.J.; Bos, J.W.; Visser, C.; Mueller, W.; Tommassen, J.; Verr
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A;Cross-references: EMBL:X70354
C;Genetics:
                                             A; Molecule type: DNA
A; Residues: 316-358
                                                                                                                   A; Title: An accessory gene, A; Reference number: $36248;
                                                                                                                                                           R; Frenken, L.G.J.; Bos, J.W.; Vil
Mol. Microbiol. 9, 579-589, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae
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                                                                                          A; Accession:
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A; Molecule type: DNA
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MUID:94018652;
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0.45;
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RESULT 14
D65129
hypothetical 38.5 kD protein in kifb-prkb intergenic region - Escherichia coli
C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 22-Jun-2003
C;Accession: D65129
C;Accession: D65129
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-340 <STO>
A;Cross-references: GB:AE005174; NID:g12517975; PIDN:AAG58461.1; GSPDB:GN00145;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A86000
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21.2%; Pred. No. 0.
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C;Superfamily: alpha/beta hydrolase
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hypothetical protein ECs4204 [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 22-Jun-2003 C;Accession: D91154 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D91154 A;Accession: D91154 A;Accession: D9154 A;Accession: D9154 A;Accession: GB:BA000007; PIDN:BAB37627.1; PID:g13363677; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Superfamily: alpha/beta hydrolase
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A;Cross-references: GB:AE000411; GB:U00096; NID:g2367213;
A;Experimental source: strain K-12, substrain MG1655
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P45524 escherichia
P25275 pseudomonas
P39986 saccharomyc
P2088 burkholderi
P3360 oryza sativ
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Q076008 homo sapien
P27742 emericella
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Q57427 haemophilus
Q13496 homo sapien
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P08658;
01-JAN-1988
01-MAR-1989
10-OCT-2003
                                                                    SEQUENCE OF 1-118 FROM N.A.

STRAIN-IFO 3458;

MEDLINE=87100109; PubMed=3800995;

Kugimiya W., Otani Y., Hashimoto Y., Takagi Y.;

"Molecular cloning and nucleotide sequence of the lipase pseudomonas fragi.";

Biochem. Biophys. Res. Commun. 141:185-190(1986).

-i- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylg
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=IFO 12049;
STRAIN=IFO 12049;
MEDLINE=89078617; PubMed=3060375;
ADVAMA S., Yoshida N., Inouye S.;
ROYAMA S., Yoshida N. Inouye S.;
Cloning, Sequencing and expression of the lipase gene
Pseudomonas fragi IFO-12049 in E. coli.";
FEBS Lett. 242:36-40(1988).
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PIR; S15911; S15911.
HSSP, P22086; 3LIP.
TIGR; VCA0221; -.
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01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Triacylglycerol
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PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Signal; Complete proteome.
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InterPro; IPR008262; Lipase_AS.
InterPro; IPR000379; Ser_estrs.
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=296;
                                                    fatty acid anion.
SIMILARITY: BELONGS
                                      LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASLAALTTE
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238
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312
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312 L
110 C
238 C
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LACTONIZING LIPASE.
CHARGE RELAY SYSTEM (
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                  lipase).
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(BY SIMILARITY).
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                                                                            diacylglycerol
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                                                     PSEUDOMONAS
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RESULT 3
LIP_PSEGL
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Best Local S
Matches 51
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01-OCT-1994
10-OCT-2003
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ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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Pfam; PF00561; abhydrolaBe; 1.
PROSITE; PS00120; LIPASE SER; 1.
Hydrolase; Lipid degradation; Signal.
Hydrolase; Lipid degradation; POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M14604; AAA25879.1; ALT_SEQ.
EMBL; X14033; CAA32193.1; --
PIR; S02005; S02005.
HSSP; Q05489; ITAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
MEDLINE=95306500; PubMed=7786905;
Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
"Lipase from Chromobacterium viscosum: biochemical characterization
                                                                                      Frenken L.G.J., Egmond M.R., Batenb
Verrips C.T.,
"Cloning of the Pseudomonas glumae
the active site residues.";
                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS SPECIES=P.glumae; STRAIN=PG1 / CBS 322.89; MEDLINE=93119130; PubMed=1476423;
                                                                                                                                                                                                       Chromobacterium viscosum.
Bacteria; Proteobacteria; Betap
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2093 (Rel. 42, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Triacylglycerol
                                                                                                                                                                                                                                                                                                                       Q05489;
                                        SPECIES-C.
                                                                                                                                                                                                                                          Pseudomonas glumae, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR008262; Lipase_AS.
InterPro; IPR000379; Ser_estrs.
                                                   SEQUENCE OF 40-54,
                                                                                                                                                                                        CBI_TaxID=337,
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                                                                            Microbiol.
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29985 MW,
                                                    AND
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                                                    CHARACTERIZATION
                                                                              58:3787-3791 (1992)
                                                                                                                                                                                                                   Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPASE.
CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM PA1562BF0772C997 CF
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                                                                                                                           Batenburg A.M.,
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                                                                                                   lipase
                                                                                                                                                                                                                                                                                                                                                                                                  195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                   Å
                                                                                                     gene
                                                                                                                             Bos J.W., Visser C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
                                                                                                                                                                                                                      Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 277;
                                                                                                      and
                                                                                                                                                                                                                                                                     lipase)
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(BY SIMILARITY).
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Hydrolase;
SIGNAL
CHAIN
ACT_SITE
ACT_SI
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EMBL; A16323; CAA01279.1; -.
EMBL; A16323; CAA012773.1; -.
EMBL; A32021; CAA02073.1; -.
PIR; A48952; A48952
PDB; 1TAH; 31-MAY-94.
PDB; 1CVL; 01-APR-97.
PDB; 1CVL; 01-APR-97.
PDB; 1QGE; 06-MAY-99.
InterPro; IPR000073; A/b hydrolase.
InterPro; IPR0008262; Lipase_AS.
InterPro; IPR0008262; Lipase_AS.
InterPro; IPR0008262; Lipase_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.:
"The crystal structure of triacylglycerol lipase from Pseudomonas
glumae reveals a partially redundant catalytic aspartate.";
FEBS Lett. 331:123-128(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of a bacterial lipase from Chr
viscosum ATCC 6918 refined at 1.6-A resolution.";
J. Mol. Biol. 259:704-717(1996).
-i- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
-i- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
SPECIES=C.viscosum; STRAIN=ATCC 6918;
MEDLINE=96275656; PubMed=8683577;
Lang D., Hofmann B., Haalck L., Hecht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          indicating homology to the lipase from Pseudomonas glumae.";
Biochim. Biophys. Acta 1256:396-402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fatty acid anion.
COTACTON: Requires calcium.
SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
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degradation; Signal; Calcium; 3D-structure.
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A: NO LOSS OF ACTIVITY.

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E RELAY SYSTEM.
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(Rel. 32, (Rel. 32,
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                                                         STANDARD;
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36928 MW;
 Created)
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   sequence update)
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                                                            LIP PSES5
P25275;
P25275;
01-MAY-1992
01-MAY-1992
10-OCT-2003
Lipase precu
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InterPro; IPR000979; Ser_estre.
InterPro; IPR000979; Ser_estre.
InterPro; IPR000952; UPF0017.
Pfam; PF00561; ahhydrolase; 1.
PROSITE; PF01133; UPF0017; 1.
PROSITE; PF01133; UPF0017; Transmembrane; Complete proteome.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 147
164
POTENTIAL.
SEQUENCE 340 AA; 38495 MW; 7DB8BA6795CBA64D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 Pseudomonas sp. (strain KWI-56)
Bacteria; Proteobacteria.
NCBI_TaxID=311;
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STRAIN=K12 / MG1655;
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Enterobacteriaceae; Escherichia.
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                                                            -1992 (Rel. 22, Created)
-1992 (Rel. 22, Last sequence update)
-2003 (Rel. 42, Last amotation update)
precursor (EC 3.1.1.3) (Triacylglycerol
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                                                                                                                                               STANDARD;
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Pred. No. 0.46
27; Mismatches
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Best Local S
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R HSSP; P22088; 3LIP.
InterPro; IPR000073; A/b hydrolase.
InterPro; IPR000279; Lipase AS.
InterPro; IPR000279; Ser_estrs.
Pfam; PF00561; abhydrolase; 1.
PROSITE; P500120; LIPASE SER; 1.
Hydrolase; Lipid degradation; Signal.
SIGNAL
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                                                                                                                                                                                                                        P39986;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
10-OCT-2003 (Rel. 42, Last ann
Probable cation-transporting A
SPF1 OR YELO31W.
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SEQUENCE
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HSSP;
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-I- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Fukase T.;
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SEQUENCE FROM N.A., AND SEQUENCE OF 45-47.
MEDLINE=92118328; PubMed=1368739;
  STRAIN=S288c / AB972;
MEDLINE=97313264; PubMed=9169868;
Dietrich F.S., Mulligan J.T., Hem
Araujo R., Aviles E., Berno A., B.
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=4932;
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131
286
330
364
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131 C.
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37511 MW;
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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Pred. No. 1.
                          Hennessy K.M.,
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Mismatches
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       Brennan
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  , Yelton M.
Carpenter
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JAME 4508

*IR; S50428; S50428.

Germonline; 139035; -...

DR GG; GG:0007579; SPF1.

DR GG; GG:0005789; C:--

TR GG; GG:0015667

R GG; GG:0007
  R GO; GO:005789; C:endoplasmic reticulum membrane; IDA.
R GO; GO:0015662; F:ATPase activity, coupled to transmembrane m.
GO; GO:0006874; P:calcium ion homeostasis; IMP.
R GO; GO:0006486; P:protein amino acid glycosylation; IMP.
R InterPro; IPR001577; ATPase E1-E2.
R InterPro; IPR008250; E1-E2_ATPase_reg.
R InterPro; IPR008254; Hydrolase.
R InterPro; IPR008544; P-ATPase-V.
R InterPro; IPR006544; P-ATPase-V.
R InterPro; IPR006544; P-ATPase-V.
R InterPro; IPR006544; P-ATPase-V.
R InterPro; IPR006547; ATPase; 1.
R PRINTS; PR001129; CATATPASE.
R PIGRPAMS; TIGR01494; ATPASE_E1_E2; 1.
R PROSITE; PS001544; ATPASE_E1_E2; 1.
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Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "P-type ATPase spf1 mutants show killer toxin SMKT.";
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Inicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.
In D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
IC., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Ith V., Taylor P., Wei Y., Botstein D., Davis R.W.,
he nucleotide sequence of Saccharomyces cerevisiae chromosome V.",
ture 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Microbiol. 32:813-823(1999).

CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the cation transport ATPases
ATPases). Subfamily v.
                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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730421
 PubMed=10361284;
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            CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                               POTENTIAL.
EXTRACELLULAR
                                                                        CYTOPLASMIC (POTENTIAL)
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RESULT 7
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P22088;
01-AUG-1991
01-FEB-1996
10-CCT-2003
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SEQUENCE
                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                            MEDLINE=97184685; PubMed=9032074;
Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H. Schnid R., Schomburg D., Rydel T.J., Oliver J.D., Strickland Schnad R., Schomburg D., Rydel T.J., Oliver J.D., Strickland Dunaway C.M., Larson S.B., Day J., McPherson A.;
"The open conformation of a Pseudomonas lipase.";
Structure 5:187-202(1997).
-I- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglyce-fatty acid anion.
-I- COPACTOR: Requires calcium.
-I- COPACTOR: Requires calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-FEB-1996 (Rel. 33, Last seq
10-OCT-2003 (Rel. 42, Last ann
Lipase precursor (EC 3.1.1.3)
                                                                                                                                                                                                                                                                                                                                      Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W., "The crystal structure of a triacylglycerol lipase fropacia reveals a highly open conformation in the abs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE STRAIN=DSM 3959; MEDLINE=91100343; PubMed=1987151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderia cepacia (Pseudomonas
Bacteria; Proteobacteria; Betaprot
Burkholderiaceae; Burkholderia.
EMBL; M58494;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Joergensen S., Skov K.W., Diderichsen B.; "Cloning, sequence, and expression of a lipegacia: lipase production in heterologous
                                                                                                                                                                                                                                                                                    K-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                                                               Structure
                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol.
                                                                                                                                    LIPASE FAMILY.
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AAA50466.1;
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                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9032073;
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Betaproteobacteria; Burkholderiales;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notation update)
(Triacylglycerol
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                                                             There are no restrictions in as its content is in
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lipase gene from Pseudomonas
ous hosts requires two
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                                     http://www.isb-sib.ch/announce/
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absence of a bound
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SIGNAL
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; 2LIP; 12-MAR-97.
; 3LIP; 16-JUN-97.
; 1HQD; 22-AUG-01.
; 4LIP; 19-AUG-98.
34;
     Similarity
                                                                                                                                                                                                                                                                                                                 PS00120;
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                   Conservative
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                                                                                                                                                                                                                                                                                                           bhydrolase; 1.
; LIPASE_SER; 1.
degradation; Signal;
                   362
364
37494 MW;
                                 9.1%; Score 85.5; DB 1; Length 364; 27.4%; Pred. No. 3.7; tive 20; Mismatches 43; Indels 2
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                    CRC64;
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     GO; GO:0016020; C:membrane; IMP.
GO; GO:0016020; C:membrane; IMP.
GO; GO:0016020; F:ATPase activity, coupl
InterPro; IPR006403; ATPase-IB_Cu;
InterPro; IPR0016416; ATPase-IB_Evy.
InterPro; IPR001756; Cu_ATPase
InterPro; IPR001756; Cu_ATPase reg.
InterPro; IPR001756; E1-E2 ATPase reg.
InterPro; IPR006121; HeavyMe_transpt.
InterPro; IPR006121; HeavyMe_transpt.
InterPro; IPR006121; HeavyMe_transpt.
InterPro; IPR005134; Hydrolase.
InterPro; IPR005194; Metal_bind.
pfam; pr00122; E1-E2_ATPase; 1.
pfam; pr00123; HMA; 1.
pfam; pr007024; Hydrolase; 1.
prints; pr007032; Hydrolase; 1.
prints; pr007033; CATATPASE.
prints; pr00943; CATATPASE.
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GermOnline; 138838; -.
SGD; S0000499; PCA1.
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TIGR01511; ATPase-IB1_Cu;

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ID ATULYEAST
AC 938360;
DT 01-OCT-1994 (
DT 01-OCT-2003 (
DT 10-OCT-2003 (
DE Saccharomycee (
OC Saccharomycee (
OC STRAIN-5288c)
RX MEDLINE-5274
RA RAM M.R., Kill
RAT RAM M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wad M.R., Kirchrath L., Hollenberg C.;
"A putative P-type Cu(2+)-transporting of Saccharomyces cerevisiae.";
Yeast 10:1217-1225(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Probably involved in copper transport and regulation of cellular copper level.
-i- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+)(In) = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=S288G;
MEDLINE=95274324; PubMed=7754711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPases). Subfamily IB. SIMILARITY: Contains I HMA domain.
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Z36164; CAA85260.1; -.
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PROSITE; F
PROSITE; F
                                            STRAIN=cv. Indica-IR36;
Reimmann C.; Mauch F., Dudler R., Hofmann C.;
Characterization of a rice gene induced by Pseudon syringae: requirement for the bacterial lema gene f Physiol. Mol. Plant Pathol. 46:71-81(1995).

-INDUCTION: By infection of leaves with certain
                                                                                                                                                                                                        Oryza šativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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Oryza sativa (
                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sec
10-OCT-2003 (Rel. 42, Last ann
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                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Indica-IR36;
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                                                                                                                                                                                      CBI_TaxID=4530;
syringae pv syringae.
SIMILARITY: DISTANT RELATIONSHIP WITH TYPE-B
CARBOXYLESTERASE/LIPASE FAMILY.
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13; Conservative
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PS01047;
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TIGR01494; ATPase P-type; 2.
PS00154; ATPASE B1 B2; 1.
PS01047; HMA_1; FALSE NEG.
PS50846; HMA_2; 1.
PS50846; HMA_2; 1.
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1182
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Pred. No.
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MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
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Best Local
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Q9PJY1;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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EMBL; Z34270; CAA84024.1; -.
PIR; S47087; S47087.
HSSP; P52704: 1077
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                                                                                                                                                                           Chlamydia muridarum.
Bacteria; Chlamydiae;
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                            CHLMU
                              "Genome sequences of Chlamydia trachomatis pneumoniae AR39.", Nucleic Acids Res. 28:1397-1406(2000).
                                                                         Read T.D., Brunham R.C., Shen C., Gill S.R., White O., Hickey E.K., Peterson J., Utterback Linher K., Weidman J., Khouri H., Craven B., Gwinn M., Nelson W., DeBoy R., Kolonay J., M. Bisen J., Fraser C.M.;
                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MOPD / Nigg;
MEDLINE=20150255; PubMed=10684935;
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PMPC OR TC0695
         (Potential).
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InterPro; IPR000379; Ser_estrs.
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47; Conserv
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268 /
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
ter membrane protein pmpC precur
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246 E
28835 MW;
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Pred. No. 7;
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BY SIMILARITY.
BY SIMILARITY.
BY 9F4E67E1216560A1
            PMP
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           outer membrane
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precursor
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           protein family.
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                                                                    Chlamydia
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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Best Local S
Matches 47
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Q976U5;
28-FEB-2003
28-FEB-2003
10-OCT-2003
                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-JCM 10545 / 7;

MEDIINE-21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukni S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;

Complete genome sequence of an aerobic thermoacidophilic

Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (
n-acetyl-glutamate semialdehyde dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006315; Autotransport.
InterPro; IPR003368; Chlamydia PMP.
Pfam; PF02415; Chlamydia PMP; 2.
TIGRFAMS; TIGR01414; autotrans barl; 1.
TIGRFAMS; TIGR01376; POMP_repeat; 8.
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                      Sulfolobus tokodaii.
                                            Res. 8:123-140(2001).

CAMPALYTIC ACTIVITY: N-acetyl-L-glutamate 5-sen

CAMPALYTIC ACTIVITY: N-acetyl-L-glutamyl phosphate +

+ phosphate = N-acetyl-5-glutamyl phosphate +

PARHWAY: Arginine biosynthesis; third step.

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

SIMILARITY: Belongs to the NAGSA dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                         OR ST0195
   SWISS-PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHVVAIGSPLQGASIVNKIEQL-GLGVALGNSAEFGLKEHDDESRYPQKSGSIAGTI--P 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSPÍTNODSÁSSHVÁÍ FRSI AASSSOSNSENI PNADGSTSAGGDAGSSSOPSTPGSDSSI
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1460 AA;
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 8
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 copyright.
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                                                the NAGSA dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.5;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                             5-semialdehyde
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 a collaboration
                                                Subfamily
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OM40_HOMAN
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ID OM40_HOMAN
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AC 09600
DT 16-00
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

MEDILINE=99449047, PubMed=10520737;

Freitas E.M., Zhang W.J., Lalonde J.P.,

Ashworth L.K., Van Bockxmeer F.M., Dawk

"Sequencing of 42kb of the APO E-C2 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM40_HUMAN STANDARD; PRT; 361 AA.
096008; Q86VW4; Q8WY09; Q8WY10; Q9BW95;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable mitochondrial import receptor subunit TOM40 homolog
(Translocase of outer membrane 40 kDa subunit homolog) (Hayma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP000981; BAB65152.1; ALT_INIT.
HAMAP; MF 00150; -; 1.
InterPro; IPR000706; AGPR_act_site.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
PRODOm; PD003765; AGPR_act_site; 1.
PROSITS; P501224; ARGC; FALSE NEG.
ARGCITS: P501224; ARGC; FALSE NEG.
ARGITIE 150 DSYMBLERS: NADP; Complete |
ARGITIE 150 BY SIMILARITY.
TISSUE=Lymphocytes;
MEDLINE=21610875; PubMed=11745481;
Das B., Tao S.-Z., Mushnitsky R., Norin A.J.;
"Genetic identity and differential expression
human malignant and non-malignant cells.";
Int. J. Cancer 94:800-806(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMF
the European Bioinformatics Institute. There are no restri-
use by non-profit institutions as long as its content i
modified and this statement is not removed. Usage by and
entitles requires a license agreement (See http://www.isb-si
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              Yoshiura K., Murray J.C.;
"A transcriptional map in the region
"A cranscriptional map in the region
sequencing and exon trapping.";
Submitted (JAN-1998) to the EMBL/GenE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein) (p38.5).
TOMM40 OR TOM40 OR PEREC1.
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                            SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                   "Sequencing PEREC1.";
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Primates;
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tay G.K.,
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GO; GO:0005741; C:mitochondrial outer membrane; NAS.
GO; GO:0005839; P:mitochondrial transport; NAS.
GO; GO:0006839; P:protein-mitochondrial targeting; NAS.
InterPro; IPR001925; Porrin Euk.
Pfam; PF04459; Euk porin; I.
Transport; Protein transport; Mitochondrion; Outer membrane; Alternative splicing. -> KGLGSPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                      VARSPLIC
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
TISSUE=Eye, Lung, Skin, Testis, and U
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=096008-2; Sequence=VSP_008589, VSP 008590; Note=No experimental confirmation available; SIMILARITY: Belongs to the Tom40 family.
                                                                                                                                                                                                                                                                                            L; AF043251; AAC82343.1; J

(AF043252; AAC82343.1; J

(L; AF316399; AAL46625.1;

(AF316399; AAL46625.1;

(AF316401; AAL46627.1;

(BC001779; AAL401779.1;

(BC001779; AAH01779.1;

(BC001719; AAH01779.1;

(BC001719; AAH01719.1;

(BC001719; AAH01719.1;

(BC001719; AAH106413.1;

(BC017224; AAH17214.1;

(BC017224; AAH17224.1;

(BC017224; AAH17224.1;

(BC017224; AAH17224.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF043253; AAC82343.1;
AF043251; AAC82343.1;
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                      361
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/FTId=VSP_008589.
Missing (in isoform
/FTId=VSP_008590.
                                                                                    SVDSNWIVGATLE
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                                                                                                                          Outer membrane;
                                                                                    KGLGSPTRETGRR
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RESULT 13
ACVS_EMAN
ACVS_EACH
ID ACVS_E
AC P27742
DT 01-AUG
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Best Local S
Matches 43
                                                                                                                                                                                                            Maccabe A.P., van Liempt H., Pallissa H., Unkles S.E., Riach M.B.R., Pfeifer E., von Doehren H., Kinghorn J.R.;

Pfeifer E., von Doehren H., Kinghorn J.R.;

"Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase from Aspergillus nidulans. Molecular characterization of the acvA gene encoding the first enzyme of the penicillin biosynthetic pathway.";

J. Biol. Chem. 266:11264-12654 (1991).

-I- FUNCTION: Bach of the constituent amino acids of the tripeptide acv are activated as aminoacyl-adenylates with peptide bonds formed through the participation of amino acid thiolester intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N-(5-amino-5-carboxypentancyl)-L-cysteinyl-D-valine synthase
(EC 6.3.2.26) (Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; En
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91286299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetase) (ACV synthetase) (ACVS).
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                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.,
                                                                                               PATHWAY: Biosynthesis of penicillin and cephalosporin PTM: The N-terminus is blocked. SIMILARITY: Belongs to the ATP-dependent AMP-binding
                                                                                                                                                      CATALYTIC ACTIVITY: L-2-aminohexanedioate + L-cysteine + L-valine + 3 AFP = N-[L-5-amino-5-carboxypentanoy1]-L-cysteiny1-D-valine 3 AMP + 3 diphosphate.

COFACTOR: Contains 3 covalently bound phosphopantetheines
                                                                      SIMILARITY: Contains 3 acyl carrier domains
                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMENI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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LVAHYLQSITPCLALGGELVYHRRPGEEGTVMSLAGKYTLNNWLATVTLGQAGMHATYYH
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361 AA;
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219
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37893
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Emericella.
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Pred. No. 12; Mismatches
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                                  a collaboration -
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-valine +
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Usage

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RESULT 14
YCSE BACSU
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Best Local Similarity
Matches 42; Conserv
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10-OCT-2003
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Pfam; PF00668; Condensation; 3.
Pfam; PF00950; pp-binding; 3.
Pfam; PF00975; Thioesterase; 1.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00012; PHOSPHOPANTETE
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DOMAIN
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REPEAT 321 910
REPEAT 1413 1993
REPEAT 2494 3078
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                 SEQUENCE FROM N.A
STRAIN=168;
                                                     Akagawa E., Kurita K., !
Submitted (SEP-1994) to
                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat.
Hypothetical protein ycsE.
YCSE OR BSU040440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensatn.
InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppantne_S.
InterPro; IPR000379; Ser_estrs.
InterPro; IPR001031; Thioesterase.
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HSSP; P14687; 1AMU.
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     MEDLINE=97124189; PubMed=8969502
                                                                                                                                  Bacillus subtilis.
Bacteria, Firmicutes;
                                                                              SEQUENCE FROM N.A.
STRAIN=168;
                                                                                                                                                                                                                                           YCSE_BACSU
                                                                                                                     CBI_TaxID=1423;
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; PS00455; AMP BINDING; 3.
; PSS0075; ACP DOWAIN; 3.
Antibiotic biosynthesis; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                    LSFKIHEVFGRTISVS-----ALFRHRTIESLAH----LIMMNVGD-----IQE 2010
                                                                                                                                                                                                                                                                                                            AGTIPLGLRSLLLRDPLDSDGT-----VTVEETKIAGMTDHIAIST 178
                                                                                                                                                                                                                                                                                                                                                                ITPVDYDNRKKIAVSPAQERLLFIHELE--GGGNAYNIDAAFELPPYIDQSRVEEALYTI
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                                                     Sugawara T., Nakamura K., the EMBL/GenBank/DDBJ dan
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DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
THIORSTERASE (BY SIMILARITY).
B MW; CB66B6D232A58CB0 CRC64;
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Pred. No. 1.7e
%1; Mismatches
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                                                                                                                                     Bacillaceae; Bacillus
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STREET RESERVATION OF 
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RX KINSE =9044033; PubMed=9384377;
RA KINSE =9044033; PubMed=9384377;
RA KINSE F. Ogsaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hasono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurlta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurlta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurlta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurlta K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurlta K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Rieger M., Rivolta C., Rocha E., Roreol B., Rase M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Rore B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Schiguchi J., Sekowska A., Sercor S.J., Sercor P., Shin B.S., Soldo B.,
RA Schiguchi J., Sekowska A., Sercor S.J., Sercor P., Shin B.S., Soldo B.,
RA Ninters P., Wajat A., Yanamoto H., Vannier F., Vassarotti A.,
RA Winters P., Watsarotti A., Wedler H., Weitzenegger T.,
Ra Katsuchi M., Tanki T., Tanka T., Terps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256 (1997)
-:- SIMILARITY: BELONGS (B.SUBTILIS) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
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Subtilist; BG11226; ycsE.
InterPro; IPR003757; ATPase_E1-E2.
InterPro; IPR003737; HAD_SF_IIB.
InterPro; IPR003834; Hydrolase.
InterPro; IPR003150; Hypothet_cof. PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
Hypothetical protein; Complete
SEQUENCE 249 AA; 28068 MW; Pfam, PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
TIGRPAMS; TIGR00099; Cof-subfamily;
TIGRPAMS; TIGR01484; HAD-SF-IIB; 1. EMBL; D38161; BAA07356.1; -.
EMBL; D50453; BAA09035.1; -.
EMBL; D50453; BAA09031.1; -.
EMBL; Z59106; CAB12212.1; -.
PIR; I39893; I39893.

9

Query Match Best Local S Matches 24

ch 8.4%; Solimilarity 26.4%; Polimilarity 26.4%; Poliminarity 22;

Score 79; Pred. No.

DB 1; Length 249

Mismatches

18;

Gaps

4

proteome. C6D420A8EC08C557 CRC64;

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RESULT 15
Y963_MYCTU
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"Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Harnsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544 (1998).
                                                                                                                                                                                                                                        MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Bryor M., Duthy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-i- SIMILARITY: SOME, TO M.TUBERCULOSIS RV2079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Hypothetical protein Rv0993c/MT0992/M50988c.
RV0963C OR MT0992 OR MT0Y10D7.11 OR MB0988C.
EMBL; Z79700; CAB02008.1; -.
EMBL; AE006983; AAK45240.1; -.
EMBL; BX248337; CAD93849.1; -.
                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as locontent
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter Fleischmann R.D., Alland D., Eisen J.A., Carpenter
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=M.tuberculosis; STRAIN=H37Rv; MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
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                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=M.bovis; STRAIN=AF2122/97;
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R.G.;
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Best Local S
Matches 42
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Hypothetical protein; Complete proteome.
SEQUENCE 266 AA; 28069 MW; E1FA43081A6B61AD CRC64;
                                                                                                                                                                                                                                                                PIR; A70718; A70718.
TIGR; MT0992; -.
 222
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                                                                              77 SRAPSCETLSHVVAIGSPLQGASIVNKIEQLGLGVALGNS-AEFGLKEHDDESRYPQKSG
                                                                                                                                                                               Similarity 26.2%; Pred. No.
                                                                                                             LGYDAPDGLKDVMHDWSARDAAGPLNRFDKGLAATTNVSDQHITAFGHSYGSLVTSLALQ
                                                                                                                                      LGYRT----QTISYNSLAIDDEAIFRRLDRSL---THASPNALV--GHSLGGLVIKRYLE
                             SIAGTIP-----
                                                     QGAP----VSDVVLYGSP--GTELTHASQ---LGVEPGHAFYMIGVNDH----
-VANTIPEFGAFGSAPQDVPGMTQLSVNTGLAPGPLLGDG
                                                                                                                                                                   Conservative
                                                                                                                                                                ; Pred. No. 9.3;
19; Mismatches
                            -----LGLRSLLLRDPLDSDG
                                                                                                                                                                                            DB 1; Length 266;
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260
                                                                                                                                                                  48;
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Search completed: April 29, 2004, 11:36:01 Job time : 35 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_vortebrate:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifie
15: sp_bacteriap:*
16: sp_bacteriap:*
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936
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Gapop 10.0 , Gapext 0.5
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sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	15	14	13	12	11	10	9	80	7	6	Ŋ	4	ω	N	ы	No.
103.5	104.5	105.5	105.5	107	111.5	112.5	121.5	136	136.5	155	170.5	179.5	532	566.5	577.5	Score
11.1	11.2	11.3	11.3	11.4	11.9	12.0	13.0	14.5	14.6	16.6	18.2	19.2	56. 8	60.5	61.7	Match Length
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16	16	16	16	16	N	16	16	16	16	N	5	16	16	9 H	16	8
P73372	Q92XY1	Q8UKB1	Q98JB5	Q98KT5	Q8KU33	С ВРННЗ	Q55748	Q8PHU7	Q7UNU3	087026	Q89SS7	Q8P6E2	Q9KN73	Q87GR6	Q8D5U8	Ħ
P73372 synechocyst	Q92xy1 rhizobium m	Q8ukb1 agrobacteri	Q98jb5 rhizobium l	Q98kt5 rhizobium l	Q8ku33 legionella		Q55748 synechocyst	Q8phu7 xanthomonas	Q7unu3 rhodopirell	087026 vibrio chol	Q89se7 bradyrhizob	Q8p6e2 xanthomonas	vibric	Q87gr6 vibrio para	Q8d5u8 vibrio vuln	Description

45	44	43	42	41	40	39	ω 8	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
90	90.5	90.5	91	91	91.5	92	92.5	92.5	93	93.5	94	94.5	94.5	94.5	94.5	95	95		95.5		96	96.5	96.5	97	97	97	99.5	102.5
9.6	•			٠	9.8	٠		9.9	٠	10.0	10.0	0	10.1	10.1	10.1	10.1		10.2	10.2	10.2	•	•	10.3	0		.0	10.6	
195	300	286	266	242	344	290	284	258	302	336	332	340	338	261	259	262	255	340	340	340	327	309	309	623	309	293	211	256
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Q7U656	Q92D71	Q82HP7	Q89R93	Q9FF27	Q7T314	Q9S295	Q9KQL2	Q81EC2	Q8DA61	Q7ZTM6	Q916C6	Q7UAR6	Q7X568	9NX680	02MX8Q	Q7UQF1	QBUKN4	Q83JB6	Q8FCX8	Q8X873	Q9ZBN4	Q9HUZ7	P72172	Q8F4V3	Q87QG8	Q9EV86	QBYX63	Q89ML2
Q7u656	Q92d71	Q82hp7	Q89r93	Q9ff27	Q7t314	Q9s295	Q9kq12	Q81ec2		Q7ztm6	Q916c6	Q7uar6	Q7x568	Q89xn6	Q8xwz0	Q7uqf1	Q8ukn4	Q83jb6	Q8fcx8	Q8x873	Q9zbn4		P72172	Q8£4v3	Q87qg8	Q9ev86 ;	Q8yx63	Q89m12
synechococc			-			streptomyce	vibrio chol	bacillus ce		xenopus lae			a			. rhodopirell			escherichia (pseudomonas		leptospira	vibrio para	pseudomonas	anabaena sp	bradyrhizob

ALIGNMENTS

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1 MQIILVHGLYMHGLVMHPLSHRLHXLGYRTQTISYNSLAIDDEAIFRRLDRSLTHASENA 60 -	Query Match 61.7%; Score 577.5; DB 16; Length 215; Best Local Similarity 64.6%; Fred. No. 1.2e-45; Matches 113; Conservative 28; Mismatches 33; Indels 1; Gaps 1;	InterPro; iPROUG'9'; Ser estrs. Hydrolase; Transferase; Complete proteome. SEQUENCE 215 AA; 23875 MW; SAD7E9FE1B690E2E CRC64;	GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA.	lete genome sequence o tted (DEC-2002) to the AE016810. AAC07731 1:	MCP6;	Vibrionaceae; Vibrio. NCBI_TaxID=672; [1] SEQUENCE FROM N.A.	se/hydro	QBD5U8; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	UT 1 UB QBD5UB PRELIMINARY; PRT; 215 AA.

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121

LKEHDDESRYPOKSGSIAGTIPIGLRSLLLRDPLD-SDGTVTVEETKIAGMTDHI 174

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Matches 110;
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN=E1 Tor N16961 / Serotype O1;

STRAIN=E20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nalson W.C., Clayton R.A., Gwinn M.I.

Dodson R.U., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.U., Haft D.H., Hickey E.K., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle:

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle:
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01-OCT-2000
01-OCT-2003
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Lancet 361:743-749(2003)

EMBL; APO05088; BAC62592.1; -. GO:0003824; F:catalytic activity; IEA.

InterPro; IPR000379; Ser_strivity; IEA.

Hypothetical protein; Complete proteome.

EYBOLENCE 205 AA; 22594 MW; FF89AEZDC67A2539 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio parahaemolyticus.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                    NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>LNKHHDAWAFPQKLGSTAGTVPTGARPLLTRNDNTMSDGTVTVEETRLDGMQDHTEVKQT</u>
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l protein.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           protein VCA0092
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Pred. No. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                             Gwinn M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205;
                                       Sellers White O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                              ۳.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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Query Match Best Local S Matches 57

Similarity

Conservative

19.2%; bu-31.8%; Pre

Score 179.5; DB 1 Pred. No. 1.2e-08; 9; Mismatches 86

DB 16;

Length

7;

Gaps

4.

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RESULT 4

QRP6

QRP6

ID QRP6

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                                                                                                           X MEDINE-2022145, PubMed=10024217;
X MEDINE-2022145, PubMed=10024217;
X MEDINE-2022145, PubMed=10024217;
X da Silva A.C.R., Ferro J.A., Rainach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
A Alves L.M.C. do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
A Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Faria J.B., Ferreira A.J.S., Jenes B.C., Mont M.F.,
A Cicarelli R.M., Kishi L.T., Leite R.P., Lemos B.G.M., Jemos M.V.F.,
A Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Mont D.H.,
A Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
A Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
A Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Setubal J.C., Kitajima J.P.,
"Comparison of the genomes of two Xanthomonas pathogens with differing Not specificities.",
17.1616/10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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Q8P6E2;
01-OCT-2002
01-OCT-2002
01-OCT-2002
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GO; GO:000382; F: catalytic activity; IEA.
InterPro; IPR000379; Ser_estre.
Hypothetical protein; Complete proteome.
SEQUENCE 209 AA; 23154 MW; 4747B6B8E54DA08E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salzberg S.L., Smith H.O., Colwell
Fraser C.M.;
"DNA sequence of both chromosomes
cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 33913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical XCC3028.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
EMBL; AE004352; AAF96006:1;
                               Hypothetical
                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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e 417:459-463(2002).
AB012415; AAM42299.1; -.
hetical protein; Complete proteome.
NCE 199 AA; 20895 MW; 2E671047AE861570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKEHDDESRYPOKSGSIAGTIPLGLRSLLLRDPLDSDGTVTVEETKIAGMTDHIAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQLHQDSWELPORLGCIAGTLRFGFRPILLGGSGMCDGTVTVAETQISGMTDHLLL
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! (TrEMBLrel. 22, L:
! (TrEMBLrel. 22, L:
! protein XCC3028.
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22, Last sequence update)
22, Last annotation updat
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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1.9e-41;
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                                                                                                                                                                                                                                                R.I.D.,
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RESULT 6
087026
ID 0870
AC 0870
DT 01-N
DT 01-N
DT 01-N
DT 210x
GN Z10x
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Best Local S
Matches 57
                                            087026
087026;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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Q89SS7;
01-JUN-2003
01-JUN-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
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MEDLINE-22484998; PubMed-12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashi
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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01-JUN-2003 (Trembirel.
01-OCT-2003 (Trembirel.
Z10r protein.
Z10R.
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GO; GO:0003824; F:catalytic activity;
GO; GO:000379; Ser_estrs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.;
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224 AA;
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                                                                                                                                                                                                                                                                             STMLAGMTDHVVVKAS 198
                                                                                                                                                                                                                                                                                                     ETKIAGMTDHIAISTT 179
                                                                                                                                                                                                                                                                                                                                                                          GPAGLELTTPATAPNALPAID----YP--VGVIAGNRFIDPVAGLEVLPKPNDGRVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKIEQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVLLHGIARTSASLTKLERALRASGFTTLNVDYSSRSKPIAAIADDIHPAIARFAERD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IILVHGLYMHGLVMHPLSHRLHKLGYRTQTISYNS----LAIDDE---AIFRRLDRSLT
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                                               (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                   PRELIMINARY;
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Best Local S
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Matches 32
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Q7UNU3;
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
SHBL; AJ231080; CAA13122.1; -.
SEQUENCE 98 AA; 11040 MW; 4350024076808F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lo
Gloeckner F.O., Kube M., Borzym K., Heitmann
Ludwig W., Gade D., Beck A., Borzym K., Heitmann
Schlesner H., Amarn R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. RB7374.
                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete SEQUENCE 328 AA; 36089 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the marine planctomycete
                                                                                                                                                                                                                                                                                                                                                                            n 1.";
Nat1. Acad. Sci. U.S.A. 100:8298-8303(2003)
BX294146; CAD75322.1; -.
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32; Conserv
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EEAQLEG
                                 EETKIAG
                                                                                       GVALGNSA-EFGLKEHDDESRY---PQKSGSIAGTIPLGLRSLLLRDPL---DSDGTVTV
                                                                                                                                      AEFAFVGHSMGNIVTRHLIGDLQADGDPKNLLPRLKSMVMLGPPNQGAAIARRLAPTGVF
                                                                                                                                                                                                           VVLLHGLMRTDNCMKSLETKLHAEGYE-QTIRFGYASTRDSLA-ESAAALRDVLENQSSD
                                                                     GLVAGPGAMELGTRWSNVESHLATPPFPFAIVAGKV---
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Pred. No. 0.000
34; Mismatches
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Pred. No. 8.5e-07;
0; Mismatches 22;
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6FE831D70FCFEF59 CRC64;
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RC STRAIN=306 / ATCC 13902 / XV 101;

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=22022145; PubMed=12024217;

RX MEDLINE=22022145; PubMed=12024217;

RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C. Camargo L.E.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., Canavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Meddanis J., Meack C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RT Most specificities.";
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Matches 44
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01-NOV-1996 (TrEMBLrel. 01, L
01-OCT-2003 (TrEMBLrel. 25, L
Hypothetical protein slr0421.
SLR0421.
                                                                                                                                                                                                                                                                                                                                                                                                                       Q55748;
Q55748;
01-NOV-1996
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                                    SEQUENCE FROM N.A. STRAIN=PCC 6803; Tabata S.;
                                                                                                                                                                                   Synechocystis sp. (strain Bacteria; Cyanobacteria; NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         host specificities.";
Nature 417:459-463(2002).
EMBL; AE011959; AAM37996.1; -.
Hypothetical protein; Complete
SEQUENCE 180 AA; 19018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Xanthomonadaceae; Xanthom
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Kanthomonas axonopodis (pv. citrı).
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        (AUG-1995)
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L; Mismatches
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Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                             6803).
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6D0E43872694A746 CRC64;
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Calauro N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Paraga J.S., Franca S.C., Franco M.C., Frohhe M., Furlan L.R.,
A Fraga J.S., Franca S.C., Franco M.C., Frohhe M.S., Gomes S.L., Kitajima J.P.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
A Honos E.G.M., Lemos M.V.F., Loger F., Lambais M.R., Leite L.C.C.,
A Krieger J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
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Best Local
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01-OCT-2000 (
01-OCT-2000 (
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Hypothetical
XFA0032
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Plasmid pXF51.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBI_TaxID=2371;
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Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 3:109-136(1996).
EMBL; D64002; BAA10393.1; -.
PIR; S76547; S76547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the sentire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
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GO; GO:0003824;
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Kaneko T., Tanaka A., Sato
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9РННЗ
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cal protein; Complete
249 AA; 27534 MW;
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A., Sato S., Kotani H.,
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F36D75D573232008 CRC64;
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S., Kimura T.
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Ч. Yaguda
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Q8KU33,
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01-OCT-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
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                                                                                        Microbiology 148:2223-2231(2002).
EMBL; AF454864; AAM73853.1; -.
GO; GO:0003824; F:catalytric activity;
InterPro; IPR000379; Ser estrs.
SEQUENCE 254 AA; 28850 MW; 999C2E
                                                                                                                                                                                                                                                     MEDLINE=22095963; PubMed=12101309; Aragon V., Rossier O., Cianciotto N.P.;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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InterPro; IPR000379; Ser_estrs.
PROSITE; PS00120; LIPASE_SER; 1.
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GO; GO:0003824; F:catalytic activity;
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Nature 406:151-159(2000).
                                                                                                                                                                                                                             "Legionella pneumophila genes
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cal Similarity
47; Conserv
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  30; Mismatches
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                      Score 111.5; DB Pred. No. 0.035;
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23; Mismatches
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Best Local S
Matches 42
Q98JB5;
01-OCT-2001 (
01-OCT-2001 (
01-OCT-2003 (
Hypothetical
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DNA Res. 7:331-336(2000).
EMBL; AP002397; BAB48729.1;
GO; 00:003824; F:catalytic activity; IEA.
InterPro; IPR000379; Ser getrs.
Hypothetical protein; Complete proteome.
SEQUENCE 256 AA; 26643 MW; 7AC63AB6830E716C
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                                                                                                                          Q98JB5
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2001 (TIEMBLIE). 18, 1
01-OCT-2003 (TIEMBLIE). 25, 1
Hypothetical protein mll1329.
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MEDLINE=21082930; PubMed=11214968;
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(TrEMBLrel. 18, L:
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24.6%; Pred. No. 0.093;
tive 28; Mismatches
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M., Matsuno Fugimor
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Best Local S
Matches 40
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01-JUN-2002 (TrEMBLrel. 21, Las
01-OCT-2003 (TrEMBLrel. 25, Las
14, pothetical protein Atu5212.
ATU5212 OR AGR PAT 295.
Agrobacterium tumefaciens (stre
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDINE-21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chan Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin G., Rouse G., Saenphimmachak C., W.Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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EMBL, AP002998; BAB49251.1; -.

GO; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR00252; Lipase AS.

InterPro; IPR000379; Ser_estre.

PROSITE; PS00120; LIPASE_EER; 1.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete P3FE5605C548D63 CRC64;
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Bacteria; Proteobact
Phyllobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLL2018
SEQUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S.,
Qurollo B., Goldman B.S., Cao Y., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
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                                                                                                                                                                                               Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        "The genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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Proteobacteria; Alphaproteobacteria;
teriaceae; Mesorhizobium.
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    , Miller N., Blanchard M., Askenazi M., Halling C.,
                                                                                                                                                                                                                                                                                engineer
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Q92XY1
Q92XY1
ID Q92XY
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DT Q1-DE
DT Q1-D
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                                                                                                        GO; GO:0046821; C:extrachromosomal DNA; GO; GO:0003824; F:catalytic activity; II InterPro; IPR008822; Lipase AS: InterPro; IPR008822; Lipase AS: INTERPROSITE; PS00120; LIPASE_SER; 1. PROSITE; PS00120; LIPASE_SER; 1. Plasmid; Hypothetical protein; Complete SEQUENCE 243 AA; 25940 MW; 59A484BDJ
                                                                                                                                                                                                                                                                                                                                                                                Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P., Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn N. Kahn S., Keating D.H., Palm C., Peck M.C., Surzycki R., Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.; "Nucleotide sequence and predicted functions of the entire Sinorhizobium melilibti pSymA megaplasmid."; Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).

EMBL; AB007296; AAK65765.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
19-OCT-2003 (TrEMBLRel 25, Last annotation update)
Hypothetical protein RA1107.
RA1107 OR SMA2023.
RA1107 OR SMA2023.
RA1107 OR SMA2023.
Plasmid pSymA (megaplasmid 1).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobium.
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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EMBL; AE007891; AAX95583.1; -.

EMBL; AG3185; AG3185.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0048824; F:catalytic activity; IEA.

InterPro; IPR008262; Lipase AS.

InterPro; IPR008379; Ser_estrs.

IPROSITE; PS00120; LIPASE SER; 1.

Hypothetical protein; Plasmid; Complete proteome.

Hypothetical protein; Plasmid; OC586AA4578FE9AB CRC64;

SEQUENCE 288 AA; 30807 MW; OC586AA4578FE9AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A Wollam C., Allinger M., Doughty D., Scott C., Lappas Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Cielo C., Slater S.;
                                                                                                                                                      InterPro;
PROSITE; P
Plasmid; H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=382;
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Pred. No. 0.
        Pred. No. 0.15;
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Similarity

Qy 3 IIIVHGLYMHGLVMHPLSHRLHKLGYRTQTISYNSIAIDDEAIFRR-LDRSLTHASPN 59
60
Db 74 ILVGHSWGGTVITETGIDPKVAGLVYVSAL-SPDAGETTAQQYEGFAPAAEF 124
QY 120 GLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTVTVEETKIAGMTDHI 174
Db 125 VIETTKDGFGYVSPAKFKAGFAHDVSDADVAFMRDAQVPINM 166
Qy 175 AISTISYENA 184
Db 167 SAFATKLENA 176

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Result
No.
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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936
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1: /cgn2_6/ptodatta/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/Bay.PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfIles1.pep:*
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(without alignments)
397.950 Million cell updates/sec
  MQIILVHGLYMHGLVMHPLS.....KIAGMTDHIAISTTSYENAV 185
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Copyright (c) 1993 - 2004 Compugen Ltd.
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  DB
WS-09-111-556A-3
WS-08-360-758-3
US-09-252-991A-27337
WS-09-328-352-669
WS-09-107-532A-4594
WS-08-034-650-10
WS-09-49-015-10
WS-08-49-015-10
WS-08-32-412-2
US-08-978-589A-2
US-08-978-589A-2
US-09-219-120-2
US-09-219-120-2
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US-09-219-120-2
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US-09-219-252-991A-27871
US-09-252-991A-2969
US-09-134-001C-3517
US-09-134-000C-4460
US-09-134-000C-4460
US-09-134-000C-4460
US-09-134-000C-4460
US-09-134-000C-4460
US-09-131-000C-4460
US-09-131-000C-4460
US-09-071-035-188
US-09-071-035-188
US-09-071-035-188
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                                                                                                                               Sequence 3, Appli
Sequence 27337, A
Sequence 27337, A
Sequence 5069, A
Sequence 4594, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 1, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 34, Appli
Sequence 349, Appl
Sequence 349, App
Sequence 349, App
Sequence 3517, Ap
Sequence 3517
                  Sequence 29669, A Sequence 360, App Sequence 6, Appli Sequence 4460, App Sequence 1858, App Sequence 186, App Sequence 186, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
  Sequence
Appli
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; TOPOLOGY: 1i; MOLECULE TYPE: US-09-111-556A-3

protein

STRANDEDNESS: single TOPOLOGY: linear

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 37.28
REGISTRATION NUMBER: 37.28
REFERENCE/DOCKET NUMBER: 3748.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

Query Match Best Local Similarity

10.4%;

Score Pred.

97; No.

DB 3;

Length 277;

57, A 955, A 965, A 9 95, A 9 95, A 9 95, A 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	US-09-111-556A-3 Sequence 3, Application US/09111556A Patent No. 6020180 GENERAL INFORMATION: APPLICANT: Svendsen, Allan APPLICANT: Svendsen, Allan APPLICANT: Svendsen, Allan APPLICANT: Borch, Kim APPLICANT: Clausen, Mogens T TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS UNMBER OF SEQUENCES: 11 CORRESSED: No. 60201800 NO. 6020180disk of No. 6020180th America, Inc. STREET: 405 Lexington Avenue, 64th Floor STRIE: New York STATE: New York STATE: New York STATE: New York STATE: New York COUNTRY: United States of America ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Tape COMPUTER READABLE FORM: MEDIUM TYPE: Tape COMPUTER READABLE FORM: MEDIUM TYPE: Tape COMPUTER READABLE FORM: APPLICATION NUMBER: US/09/111,556A FILING DATE: 22-DEC-1994 CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:	יסיי בלסיילי יסיסיסיסיי ב
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US-08-360-758-3
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APPLICANT: Svendse
APPLICANT: Pathar,
APPLICANT: Egel-Mi
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                                                                   Best
                                                                                  Query Match
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: DK PCT/DK93/00225
APPLICATION NUMBER: DK PCT/DK93/00225
APPLICATION NUMBER: DX PCT/DK93/00225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 37.
TELECOMMUNICATION INFORMATION:
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APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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                                                                   Local
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TOPOLOGY: lir
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3 IILVHGL-------YMHGLVMHPLSHRLHKLGYRTQTISYNSLAIDDEA----IFRR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10174-6401
                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08360758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAAFNRQYPQGLPDRWGGMGPAQVNAV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QLGLGVALGNSAEFG--LKEHDDESRYFQKSGSIAGTIFLGLRSLLLRDFLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: No. 60748630 No. 6074863disk of No. 6074863th America, Inc.
405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                              212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathar, Shamkant A
Egel-Mitani, Michi
                                                     Conservative
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                                                                                                                                                         linear
                                                                                                                                                                                                                                                                             212-867-0123
                                                                                                                                     protein
                                                                                                                                                                        single
                                                 10.4%; Score 97; DB 3; 24.6%; Pred. No. 0.015; tive 31; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/360,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of America
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                                                                                                                                                                                                                                                                                                               3748.204-US
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                                                     79;
                                                                                  Length 277
                                                   Indels
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                                                   Gaps
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RESULT 3
US-09-252-991A-27337
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                                                                                                                            US-09-328-352-5069
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/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27337

                                                                                                                                                                                 FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5069
LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27337
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27337, Appli
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 5069, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                          Matches
                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR ETLING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                       APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                              TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 10.3%; Score 96.5; DB Local Similarity 27.7%; Pred. No. 0.023; Mismatches 31; Conservative 23; Mismatches
                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 LTGAEKVNLIGHSQGGMTV-RYVAGVAP--QLVASVTTMGTPHKGTPVADAV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 VAAFNRQYPQGLPDRWGGMGPAQVNAV 195
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                                          39,
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                                                           Similarity
IILVHGLYMH------GLVMHPLSHRLHK----LGYRT-QTISYNSLAIDDEAIFR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVLSHGLFGFKSVGPVDYWHAIVPALEKDGAKVFATSQSPVNSNEVRGEQLLAQVEEVLA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD--RSLTHASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKIE- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILLVHGLFGFDRIGSHHYFHG-----IKQALNECG-ASVFVPIISAANDNEARGDQLLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTHASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKI 104
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09252991A
                                                           10.3%;
                                          18; Mismatches
                                                         Score 96.5; DB Pred. No. 0.034;
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                                                                             DB 4;
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                                            42;
                                                                               Length 453;
                                            Indels
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                                            33;
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                                            Gaps
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                                                                                                                                                                                                                                      NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...316;
SEQUENCE DESCRIPTION: SEQ ID NO: 4594:
US-09-107-532A-4594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-107-532A-4594
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                        Matches
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4594:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

PILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

PILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

PILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 VILVHGLCMNHLTWSNAHYGGIGERLLAQRDHNTMLYLNYNTGRRISANGRS-----FS
113 LGNSAEFGLKEHDDESRYPQKSGSIAGTIFLGLRSLLLRDFLD----SDGTV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 IVNKIEGIGLGV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                        61 LYCHSLGGLVIKRYL-----ESRAPSCETLSHVVAIGSPLQ----GASIVNKIEQLGLGVA 112
                                                                                                                                                                           Similarity
                                                               IVGHSMGGVSALRYLGTYGQDTSLPQVQTLT---AIGAPFNDFVDDSAQSLTDELAKGPA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VLERFGFAL 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ry: Waltham
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecium
                                                                                                                                                  10.3%; Score 96; DB 4; Length 316; 31.2%; Pred. No. 0.023; ative 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (781)893-5007
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AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                        28;
                                                                                                                                                        Gaps
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US-08-034-650-10
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PRENKER, Leon G.
APPLICANT: VERRIPS, COTHELLS T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CISHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 861-3000 TELEFAX: (202) 822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1615 L. : CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 358 amino acide
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                                                                                                                                                           162
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    192
                                                                           161 --TVEETKIAGMTDHIAISTTSY 181
                                                                                                                                                                                                                                  104 IEQLGLGVALGNSAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTV--- 160
                                                                                                                                                                                                                                                                                                             105 LAYVKQVLAATGATKVNLIGHSQGGLT-SRYVAAVAP--QLVASVTTIGTPHRGSEFADF 161
                                                                                                                                                                                                                                                                                                                                                                                         46 FRRLDRSL--THASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 VILVHGLAGTDKFANVVDYWYGIQSDLQSH-----GAKVYVANLSGFQSDDGPNGRGEQL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IILVHGL-----YMHGLVMHPLSHRLHKLGYRTQTISYNSLAIDD-----EAI 45
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    SHNTDQDALAALRTLTTAQTATY 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 96; DB 1; Length 358; 21.2%; Pred. No. 0.027;
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                                                                                                                                                                   --DVLKTDPTGLSSTVIAAFVNVFGTLVSS 191
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RESULT 7 US-08-449-015-10

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RESULT 8
US-09-543-681A-6874
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US-08-449-015-10
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Best Local S
                                Sequence 6874, Applic
Patent No. 6605709
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-000
TELEPAX: (202) 822-0944
 TITLE
                 APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, Cornells T.
APPLICANT: VISSER, Christiaen
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435

RICHARD ATA:
APPLICATION NUMBER: US 07/727,235

FILING DATE: 03-UU-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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OF INVENTION: NUCLEIC
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                                                                                                                                                                                                   161 -- TVEETKIAGMTDHIAISTTSY 181
                                                                                                                                                                                                                                                                          104 IEQLGLGVALGNSAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTV--- 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                         Application
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                                                                         US/09543681A
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   ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNK/5970/91731
                                                                                                                                                                                                                                        ----DVLKTDPTGLSSTVIAAFVNVFGTLVSS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6874
LENGTH: 333
TYPE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-602-359A-38
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GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: FEBTUARY 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                          ZIP: 9203/
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMBUTTER: IBM PS/2
COMBUTTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 090
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE CITY: LA JOLLA STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 MLEPCSTKIER-----ĠFŚRFYQWYLLKĠĹKRNATRKLIRYPQ-----SLPISLLT 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 QGASIVNKIEQLGLGVALGNSAEF-----GLKEHDDES--RYPQKSGSIAGTIPLGLRS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 NSLAIDDEAIFRRIDRSLTHASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURPHY, Den
REID, John
MAFFIA, Ant
                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTSON, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 92.5; DB 4; 23.8%; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                           09010/010003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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Patent No. 6017866
; GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Gerritse, Gijsbert
APPLICANT: Lenting, Hermanus
TITLE OF INVENTION: LIPASES WITH IMPROVED
TITLE OF INVENTION: SURFACTANT RESISTANCE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-732-412-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                     PILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 942012
PILING DATE: 04-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GG30
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/732,412
FILING DATE: 22-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/0168
FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 525 Eng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                        TELEPHONE:
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                                                                                                                                                                                        EP 94201253.5
                                                                                                                                                                                                                                            PCT/EP95/01687
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                                                                                               GC307-US
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                                                                                                                                        US-08-978-589A-2
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                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYDE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,589A
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
                                                                                                   Query Match
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISHII, Takeshi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: ESTERASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                Local Similarity
nes 47; Conserv
                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040
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CITY: FALLS CHURCH
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                                                                                                                                                                                                                                                                           ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 --SLTHASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKIEQL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 IIIVHGI-----YMHGLVMHPLSHRLHKLG-YRTQTISYNSLAIDDEAIFRRLDR
                             3 IILVHGL----YMHGLVMH----PLSHRLHKLGYRTQTISYNSLAIDD------EAIFRR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGEGAYKVNGVSYYSWSGTSPLTNVLDVSDLLLGASSLTFDEP--NDGLV 260
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 iiivhgitgtdkyggvveywyripedlrah--gaavyvanlsgpqsddgpngrgeqllaf 112
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                                                                                                                                                                                                                                                            至: (703)
(703) 20
                                                                    Conservative
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O. BOX 747
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                                                                                 9.7%;
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Pred. No. 0.08;
                                                                                  Score 90.5; DB 3;
Pred. No. 0.11;
                                                                     Mismatches
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                                                                                                     Length 363;
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Sequence 1, Application US/09336601

Patent No. 6184008

GENERAL INFORMATION:
APPLICANT: OHTA, Hiromichi
APPLICANT: SUGAI, Takeshi
APPLICANT: ISHI, Takeshi
APPLICANT: ISHI, Takeshi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
FILE REFERENCE: 2185-249p
CURRENT APPLICATION NUMBER: US/09/336,601
CURRENT FILING DATE: 1998-06-21
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2
GOFFMADE: DESCRIPTION SECUENCE SERVINGS SERVINGS SECUENCE SERVINGS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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US-09-336-601-1
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US-09-219-120-2
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; ORGANISM: E. coli JM 109/pAL 612 strain
US-09-336-601-1
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SEQ ID NO 1
LENGTH: 363
Query Match 9.7%; Score 90.5; DB Best Local Similarity 26.9%; Pred. No. 0.11; Matches 47; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/219,120
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: ISHII APPLICANT: TAKESHI, ISHII APPLICANT: SATOSHI, Mitsuda TITLE OF INVENTION: ESTERASE GENE FILE REFERENCE: 20-4336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09219120 Patent No. 6472189
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                                                                                                                                         ORGANISM: Burkholderia cepacia
-09-219-120-2
                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                              LENGTH: 363
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26.9%; Pred. No. 0.11
ative 20; Mismatches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRICK APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27871
LENGTH: 344
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                        Sequence 349, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                           TITLE OF INVENTION:
COMPUTER READABLE FORM:
                               COUNTRY:
                                                                           CITY: Atlanta
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                                                                                                                                   ADDRESSEE:
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                                                      Georgia
                                                                                              2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                            David William Holden

IVENTION: Identification of Genes
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 0.3-MAY-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 436
RESERENCE/DOCKET NUMBER: REMS 101
TELEPHONE: 4040 #73-8795
SATTONNEY/AGENT IMPORMATION:
NAME: Paber: PATE AL
RESERVATION NUMBER: REMS 101
TELEPHONE: (404) #73-8795
SEQUENCE: GHARACTERISTICS:
SEQUENCE: CHARACTERISTICS:
SEQUENCE: GHARACTERISTICS:
SEQUENCE: GHARACTERISTICS
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Result
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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15 US-10-603-260-5
15 US-10-603-260-5
15 US-10-369-493-8213
15 US-10-421-654-16
10 US-09-903-410-38
10 US-10-027-805-38
14 US-10-027-804-38
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5 US-10-282-122A-76642
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US-09-938-803-20
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                  Sequence 5, Appli
Sequence 82.3, App
Sequence 16, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 10998, A
Sequence 2, Appli
Sequence 246354,
Sequence 1, Appli
Sequence 170475, A
Sequence 14086, A
Sequence 47418, A
Sequence 47418, A
Sequence 76642, A
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Sequence
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270	403	303	302	1129	587	257	240	225	1460	361	360	331	331	301	267	259	252	244	332	259	244	470	432	323	301	279	275	275	1216
12	14	12	12	14	12	12	12	12	12	10	12	12	ø	14	12	15	15	15	14	15	15	15	14	12	12	12	15	15	15
0-206-576-18	-10-156-761-1442	-10-282-122A-50	-10-282-122A-4733	-10-156-761-8	-10-425-114-6812	-10-282-122A-773	-10-425-114-4513	-10-425-13	-10-282-122A-552	-09-896-908-2	-10-424-599-22183	-10-282-122A-5	09-815-242-1079	-10-156-761	-10-282-122A-46	-10-369-493-167	-10-369-493-1986	-10-369-493-883	-10-050-882-9	-10-369-493-2	-10-289-762-	-10-421-654-	-10-156-761-1345	-10-282-122A-6435	-10-282-122A-49	-10-282-122A-6262	-10-369-493-722	-10-369-	0-369-493-150
equence 18	e 14428,	50776,	9 47335,	8946,	68123,	e 77391,	45130,	Ø	equence 55255,	e 2, Apr	e 221830	Sequence 57052, A	10799,	e 7846,	equence 4	6	equence 1	equence 8	Sequence 99, Appl	equence	equence 3	e 5	equence 13	9	e 4:	ce 6	ence 7223,	O	χ, Έ

ALIGNMENTS

RESULT 1

B &	B & B &	g Qy	Query M Best Lo Matches	CUR. CUR. NUM. SOP SEQ LE TY OR US-10-	US-10-60; ; Sequen; ; Sequen; ; GENERA; ; APPLI; ; TITLE; ; FILE;
181 YENAV 185 181 YENAV 185	121 LKEHDDESRYPÇKSGSIAGTIPIGLRSILLERDPLDSDGTVTVEETKIAGMTDHIAISTTS 180		Query Match 100.0%; Score 936; DB 15; Length 185; Best Local Similarity 100.0%; Pred. No. 4.1e-96; Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CURRENT APPLICATION NUMBER: US/10/603,260 CURRENT FILING DATE: 2003-06-24 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Kopatentin 1.71 SEQ ID NO 5 LENGTH: 185 TYPE: PRT ORGANISM: Vibrio metschnikovii RH530 US-10-603-260-5	US-10-603-260-5 Sequence 5, Application US/10603260 Publication No. US20040009570A1 GENERAL INFORMATION: APPLICANT: CJ Corporation TITLE OF INVENTION: An alkaline lipase from Vibrio metschnikovii RH530 and a TITLE OF INVENTION: nucleotide sequence encoding the same

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION NUMBER: WITH IMPROVED PROPERTIES
PILE REPPERANCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEG ID NOS: 47374
SEQ ID NO 8213
LENGTH: 249
TYDE: PRI
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US-10-421-654-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Thermobifida fusca US-10-369-493-8213
                                                                                     ; FEATURE:
; OTHER INFORMATION: Obtained from US-10-421-654-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-8213
Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10421654
Publication No. US20040005604A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8213, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                 FILE REFERENCE: 09010-094001
CURRENT APPLICATION NUMBER: US/10/421,654
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US 60/374,313
PRIOR FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gramatikova, APPLICANT: Hazlewood,
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Barton, Nelson R.
TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                             TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                          ENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 DEL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 NKI 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 AIFRELDRSLT--HASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 VVLVHGYGEHIGRYEHVARWLCEHGAVCYGVDHRGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 29.3
36; Conservative
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            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 110; DB 15; 29.3%; Pred. No. 0.0011;
                           10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svetlana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Mismatches
          ; Score 97; DB 15; Pred. No. 0.075; 36; Mismatches
                                                                                                             an environmental sample
                                                   DB 15; Length 447;
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               Indels
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            50;
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            Gaps
               13;
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US-09-903-410-38
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                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
SEQ ID NO 38
LENGTH: 262
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR FILING DATE: 1999-08-24
PRIOR PPLICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DIVERSA CORPORATION APPLICANT: ROBERTSON, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1180-2
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Thermococus CL-2-30LC
                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RSMIGRVTKGWKGTRLFETGKHILKGLELASPYAWALAERDLFSDQNYY--GAGRILCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 LVGNAGYRGISAVANRP-GTDGTVRVSSANL 208
161
                                  151 RDPLDSD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 WSDRGLPTAPRSVDAVV-HSTGGLVIRDWLTQLYTPETAPIRRLLMLAPANFGSPLAHTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 -- DRSLTHA--SPNALVGHSLGGLVIKRYL-ESRAPSCETLSHVVAI-----GSPL--QG
                                                                                                      93 SPLQGASIVNKIEQLGLGVALGN--SAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLL 150
                                                                                                                                                                                                                 16 VVLVHGLGEHSGRYGRLIKELNYAGFGVYTFDWPGHGKSPGKRGHTSVEEAMEIIDSIIE 75
                                                                                                                                           76 EIREKPF-----LFGHSLGGLTVIRYAETREDKIRGLIASSPALAKSPETEGFMVAL-
                                                                                                                                                                              47 RRLDRSLTHASPNALVGHSLGGLVIKRYLESR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LVIIHGWSDEAGSFKTLARRLAKAPPEGLGTQVTEIHLGDYVSLDDQVTFNDLVDAMARA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IILVHGLYMHGLVMHPLSHRLHKL---GYRTQTISY---NSLAIDDEAIFRRL-----
                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                     3 IILVHGLYMHGLVMHPLSHRLHKLGYRTQTISY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLGLR----
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 EDPLVHD 167
                                                                       ----AKFLGKIAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINK, Steven
SWANSON, Ronald
WARREN, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAFFIA, Anthony
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLLRDPLDSDGTVTVEETKI 167
                                                                                                                                                                                                                                                                                                            24.6%;
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                                                                         -GVVLSNGIKPELLSRNRDAVRRY
                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                          Score 91.5; DB
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                          58,
                                                                                                                                                                                                                                                                                                                               Length 262;
                                                                                                                                                                                                                                                       -----NSLAIDDEAIF
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                                                                                                                                                                                    APSCETLSHVVAIG 92
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                                                                                                                                                 127
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US-10-027-805-38
; Sequence 38, Application US/10027805
; Publication No. US20020164725A1
; GENERAL INFORMATION:

RESULT 5

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US-10-027-805-38
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HAILE, LISA A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-509
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION UNMER: US/10/027,805
APPLICATION NUMBER: US/10/027,805
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,359
FILING DATE: <Unknown>
APPLICATION NUMBER: US/602,359
APPLICATION NUMBER: US/602,359
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DIS
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ESTERASES NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROBERTSON, Daniel E.
                      APPLICANT:
                                                                                                                                                                                                                                                                              128 ----AKFLGKIAP---GVVLSNGIKPELLSRNRDAVRRY----
                                                                                                                                                                                           161 EDPLVHD 167
                                                                                                                                                                                                                                 151 RDPLDSD 157
                                                                                                                                                                                                                                                                                                                  93 SPLQGASIVNKIEQLGLGVALGN--SAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLL 150
                                                                                                                                                                                                                                                                                                                                                                                                        47 RRLDRSLTHASPNALVGHSLGGLVIKRYLESR-----
                                                                                                                                                                                                                                                                                                                                                               76 EIREKPF-----LFGHSLGGLTVIRYAETRPDKIRGLIASSPALAKSPETPGFMVAL- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VVLVHGLGEHSGRYGRLIKELNYAGFGVYTFDWPGHGKSPGKRGHTSVEEAMEIIDSIIE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IILVHGLYMHGLVMHPLSHRLHKLGYRTQTISY------NSLAIDDEAIF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 262 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%; Score 91.5; DB 13; illarity 24.6%; Pred. No. 0.14; Conservative 16; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY, John
                    ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAFFIA,
  MURPHY, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthony
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                                                                                                            RESULT 7
US-10-156-761-10998
; Sequence 10998, Application US/10156761
; Publication No. US20030119016A1
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GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619-678-5070
TELEPAX: 619-678-509
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,804
FILING DATA: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/602,359
APPLICATION NUMBER: 08/602,359
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/602,359
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HALIE, LISA A.
REGISTRATION UMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 262 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                                        161 EDPLVHD 167
                                                                                                                                                                                                                                                                                 151 RDPLDSD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 RRLDRSLTHASPNALVGHSLGGLVIKRYLESR----
                                                                                                                                                                                                                                                                                                                                                                                                             76 BIREKPF-----LFGHSLGGLTVIRYABTRPDKIRGLIASSPALAKSPETPGFMVAL- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 VVLVHGLGEHSGRYGRLIKELNYAGFGVYTFDWPGHGKSPGKRGHTSVEBAMEIIDSIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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                                                                                                                                                                                                                                                                                                                         ----AKFLGKIAP---GVVLSNGIKPELLSRNRDAVRRY--
                                                                                                                                                                                                                                                                                                                                                                  SPLQGASIVNKIEQLGLGVALGN--SAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLL 150
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STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CALIFO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 91.5; DB 14; ilarity 24.6%; Pred. No. 0.14; Conservative 16; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -APSCETLSHVVAIG 92
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10998
LENGTH: 286
TYPE: PRT
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US-10-147-467-2
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                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 363
; TYPE: PRT
; ORGANIZM: Burkholderia cepacia
US-10-147-467-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10147467
publication No. US20030027295A1
GENERAL INFORMATION:
APPLICANT: TAKESHI, Ishii
APPLICANT: SATOSHI, Mitsuda
APPLICANT: SATOSHI, Mitsuda
TITLB OF INVENTION: ESTERASE GENE AND
FILE REFERENCE: 20-4336P
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/147,467
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Best Local
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 PGSEVIEELQRPAPGCRTHFVSFWSDLDHLMDPLETACVEHPDLMVQNVRVSGI-GHLAL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || : :||||||: |:
137 HARVD-IVGHSLGGLIARYYVQCLGGDIRVRT-LVTLGTPHSGTRVAPLANAHPIVRQMR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 PVHPAVATGIRQALDSEGTGAEAAPRTDGLT 284
                                                                                                                           49 LDRSL--THASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASIVNKIEQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 QGASIVNKIEQLGLGVA------LGNSAEFGLKEHDDESRYPQKSGSIAGTIPL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 İİLVHĞLTGTDKYĞĞVVEYWYRIPEDLRAH--GAAVYVANLSGFQSDDGPNGRGEQLLAF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VVLLHGFIDNRSVFVLLRRSLTQHGRQQIESLNYSPLTCDIRTAAELLGRHIEVICERTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                ch 9.7%; Score 90.5; DB 14; Similarity 26.9%; Pred. No. 0.3; 47; Conservative 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 IILVHGLYMHGLVMHPLSHRLHKLG-YRTQTISYNSLAIDDEAIFRRLDRSLT-----
                                                                                                                                                                                                            3 IIIVHGL----YMHGLVMH----PLSHRLHKLGYRTQTISYNSLAIDD-----EAIFRR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                          LGLGVALGNSAEFGLKEHDDESRYPQKSGSIAGTIPLGLRSLLLRDPLDSDGTVT 161
                                                                                   VKQVLAATGAQKVNLIGHSQGGLT-SRYVASVAP--ELVASVTTISTPHWGSQFADFVQQ
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20.9%; Pred. No. 0.21;
rative 38; Mismatches
  --LQTDPTGLSSTVLGAFANALGTLT 194
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                                                                                                                                                                                                                                                                                               Length 363;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                       51;
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APPLICANT: HOWDEN, Maria
APPLICANT: HOWDEN, Maria
FITTLE OF INVENTION: COLLAGEN-BINDING ADHESIN FRO
FILE REFERENCE: P07136US01/BAS
CURRENT APPLICATION NUMBER: US/10/098,174
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/275,718
PRIOR APPLICATION NUMBER: 60/275,718
PRIOR PILING DATE: 2001-03-15
INUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
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US-10-098-174-1
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                                                                                                                                                      , ORGANISM: Staphylococcus epidermidis US-10-098-174-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-215323)B
FILE REFERENCE: 38-215323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 246534
LENGTH: 443
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Publication No. US20040031072A1 
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10098174
Publication No. US20020169288A1
GENERAL INFORMATION:
                                                                                                                                                                                                                       SEQ ID NO 1
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Best Local :
                                                              Query Match 9.5%; Score 88.5; DB Best Local Similarity 21.1%; Pred. No. 0.83; Matches 47; Conservative 32; Mismatches
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                                                                                                                                                                                                      TYPE: PRT
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Local Similarity 23.6%; Pred. No. 0.45;
Les 43; Conservative 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 LYLNPRIKHITGYMAPLVDSLQKLGY------ADGETLFGAPYDFRYGLAAEGHP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47
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                                                                                                                                                                                                                         518
9 LYMHGLVMH------PLSHRLHKLGYRTQTISYNSLAIDDEAIF--------
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                                                                       Indels 89;
                                                                                                              Length 518;
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US-10-282-122A-70475
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                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 70475
LENGTH: 627
TYPE: PRT
                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70475, Application US/10282122A
Publication No. US20040029129A1
                                                                          Matches
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                                                                                                                                                   ORGANISM: Staphylococcus epidermidis ·10-282-122A-70475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 CURRENT FILING DATE: 2003-07-20 PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-1
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
248 VVFVHGFV--GLVGEDAFSMYPNYWGGTKYNVKQELTKLGYRVHEANVGAFSSNYDRAVE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 VVFVHGFV--GLVGEDAFSMYPNYWGGTKYNVKQELTKLGYRVHEANVGAFSSNYDRAVE 164
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                                      IILVHGLYMHGLV-----MHP-----LSHRLHKLGYRTQTISYNSLAID-DEAI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKIEQLG----LGVALGNSAEFGLKEHDDESRYPQKSGSIAGT 140
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Zyskind, Judith
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Malone, Cheryl
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Forsyth, R.
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Trawick, John
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                                                                        Conservative
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lio, Carlos
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                                                                                             9.5%;
                                                                        32;
                                                                        Score 88.5; DB 12;
Pred. No. 1.1;
2; Mismatches 55;
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                                                                             Indels
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US-10-156-761-14086
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US-10-282-122A-47436
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14086
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                               108 LQVF--VDKVLTATGATKADLVGHSQGGMMPRYYLKF----
                                                                             179 DILISTATEGLADOVVGSAFMAKLNAGGDTVAGVHYTVIATOYDEVV
                                                                                                                                                      149 VNAL----VGIAPNNH-----
                                                                                                                                                                                         101 VNKIEQIGIGVALGNSABFGIKEHDDESRYPQKSGSIAGTIPLGIRSLILRDFIDSDGTV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 NRIGKIGGTKALDLELGFS-QWGFKQQPNES-YAEYAKRIANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 NKIEQLG----LGVALGNSAEFGLKEHDDESRYPQKSGSIAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 LYYYIKGGRVDYGAAHAAKYGHKRYGRTYEGIMPDWEPGKKIHLVGHSMGGQTIRLMEHF 365
                                                                                                                 161 TVEETKIAGMID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                    45 -- IFRRLDRSL--THASPNALVGHSLGGLVIKRYLESRAPSCETLSHVVAIGSPLQGASI
                                                                                                                                                                                                                                                                                                             53 VVLVHGTLGNSVDNWLGLAPY-LEHR----GYCVFSLDYGQLSGVPFFHGLGPIDKSAEQ 107
                                                                                                                                                                                                                                                                                                                                                 3 IILVHGLYMH-----GLVMHPLSHRLHKLGYRTQTISYNSLA-----IDDEA--
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                          23.5%;
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Pred. No. 0.45;
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Sequence 47438, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION: APPLICANT: Wang, Liangsu

APPLICANT:

APPLICANT:

Zamudio, Carlos Malone, Cheryl Haselbeck, Robert Ohlsen, Kari Zyskind, Judith Wall, Daniel

Trawick, John

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US-10-282-122A-47438
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Best Local S
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LENGTH: 364
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LAYVKTVLAATGATKVNLVGHSQGGLT-SRYVAAVAP--DLVASVTTIGTPHRGSEFADF 166
                                                                                                                                                                                                                                                                                                                                                                                                             167 VQDV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 IEQL 107
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NYENTION: Identification of Essential Genes
INVENTION: Identification of Essential Genes
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                                               Trawic...
Carr, Grant
Carr, Grant
Robert
                                                                                                                                                                               Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                  Yamamoto, Re Forsyth, R.
                                                                                                                                      Ohlsen, Kari
Zyskind, Judith
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                                                                                                 Trawick, John
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    in Microorganisms
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                                       PRIOR FILING DATE: 1999-05; NUMBER OF SEQ ID NOS: 40; SOFTWARE: PERL Program; SEQ ID NO 20; LENGTH: 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Treponema pallidum
US-10-282-122A-76642
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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Best Local :
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/11,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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                                                                                                                                                                                     APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Yang, Junming
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: FULL-LENGTH EXPRESSED GENETIC MARKERS
FILE REFERENCE: PF-0695 US
CURRENT APPLICATION NUMBER: US/09/938,803
                                                                                                                                                                                                                                                                                                                            APPLICANT: Yue, Henry
APPLICANT: Tang, Y. 7
APPLICANT: Lal, Preet
APPLICANT: Reddy, Ro
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                  CURRENT FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: 09/311,894
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NUMBER OF SEQ ID NOS: 78614
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PRIOR FILING DATE: 2000-09-09
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
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                                                                                                                                                                                                                                                                                                                                                   Tang, Y. To
                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09938803
S20020076762A1
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                                                                                                                               1999-05-14
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; Pred. No. 0.68;
26; Mismatches
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